

10/501841
DT12 Rec'd PCT/PTO 14 JUL 2004

SEQUENCE LISTING

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<120> Compositions and Methods for the Detection, Diagnosis
and Therapy of Hematological Malignancies

<130> 014058-014402PC

<140> WO PCT/US03/02353
<141> 2003-01-22

<150> US 10/057,475
<151> 2002-01-22

<160> 124

<170> PatentIn Ver. 2.1

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Pro Glu Gly Gly Thr Ile Ile Val Thr Gln Asn Arg Asn Arg Glu Arg			
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 Ile Leu Ala Arg Lys Leu Cys Glu Gly Ala Ala Asp Asp Pro Asp Ser
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 Phe Val Leu Gly Leu Phe Leu Trp Phe Leu Lys Arg Glu Arg Gln Glu
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 Glu Tyr Ile Glu Glu Lys Lys Arg Val Asp Ile Cys Arg Glu Thr Pro
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 Asn Ile Cys Pro His Ser Gly Glu Asn Thr Glu Tyr Asp Thr Ile Pro
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 35 40 45
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 Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
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 Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
 100 105 110
 Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
 115 120 125
 Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
 130 135 140
 Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
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Val Thr Ile Lys Cys Pro Leu Pro Glu Met His Val Arg Ile Tyr Leu
35 40 45

Cys Arg Glu Met Ala Gly Ser Gly Thr Cys Gly Thr Val Val Ser Thr
50 55 60

Thr Asn Phe Ile Lys Ala Glu Tyr Lys Gly Arg Val Thr Leu Lys Gln
65 70 75 80

Tyr Pro Arg Lys Asn Leu Phe Leu Val Glu Val Thr Gln Leu Thr Glu
85 90 95

Ser Asp Ser Gly Val Tyr Ala Cys Gly Ala Gly Met Asn Thr Asp Arg
100 105 110

Gly Lys Thr Gln Lys Val Thr Leu Asn Val His Ser Glu Tyr Glu Pro
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Ser Trp Glu Glu Gln Pro Met Pro Glu Thr Pro Lys Trp Phe His Leu
130 135 140

Pro Tyr Leu Phe Gln Met Pro Ala Tyr Ala Ser Ser Ser Lys Phe Val
145 150 155 160

Thr Arg Val Thr Thr Pro Ala Gln Arg Gly Lys Val Pro Pro Val His
165 170 175

His Ser Ser Pro Thr Thr Gln Ile Thr His Arg Pro Arg Val Ser Arg
180 185 190

Ala Ser Ser Val Ala Gly Asp Lys Pro Arg Thr Phe Leu Pro Ser Thr
195 200 205

Thr Ala Ser Lys Ile Ser Ala Leu Glu Gly Leu Leu Lys Pro Gln Thr
210 215 220

Pro Ser Tyr Asn His His Thr Arg Leu His Arg Gln Arg Ala Leu Asp
225 230 235 240

Tyr Gly Ser Gln Ser Gly Arg Glu Gly Gln Gly Phe His Ile Leu Ile
245 250 255

Pro Thr Ile Leu Gly Leu Phe Leu Leu Ala Leu Leu Gly Leu Val Val
260 265 270

Lys Arg Ala Val Glu Arg Arg Lys Ala Leu Ser Arg Arg Ala Arg Arg
275 280 285

Leu Ala Val Arg Met Arg Ala Leu Glu Ser Ser Gln Arg Pro Arg Gly
290 295 300

Ser Pro Arg Pro Arg Ser Gln Asn Asn Ile Tyr Ser Ala Cys Pro Arg
305 310 315 320

Arg Ala Arg Gly Ala Asp Ala Ala Gly Thr Gly Glu Ala Pro Val Pro
325 330 335

Gly Pro Gly Ala Pro Leu Pro Pro Ala Pro Leu Gln Val Ser Glu Ser
340 345 350

Pro Trp Leu His Ala Pro Ser Leu Lys Thr Ser Cys Glu Tyr Val Ser
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TCTGCTGCTG ATGAAGGTG TGTTCAAGTC AGTAGAAAGA CCATTCTTC GAATTCTTC 600
TCACCAGAGG TATTTGTGCT GCCTGTTGAT GTAGAAAAGG AAAATGCCA CTTTATGTT 660
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reading frame His tag fusion

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Ile Asp Gly Ser Pro Arg Leu Leu Asn Thr Asp His Pro Pro Cys Gln
35 40 45

Leu Asp Ile Arg Leu Met Arg His Lys Ala Val Trp Ile Asn Pro Gln
50 55 60

Asp Val Gln Gln Gln Pro Gln Asp Leu Gln Ser Gln Val Pro Ala Ala
65 70 75 80

Gly Asn Ser Gly Thr His Phe Val Thr Asp Ala Ala Ser Pro Ser Gly
85 90 95

Pro Ser Pro Ser Cys Leu Gly Asp Ser Leu Ala Glu Thr Thr Leu Ser
100 105 110

Glu Asp Thr Thr Asp Ser Val Gly Ser Ala Ser Pro His Gly Ser Ser
115 120 125

Glu Lys Ser Ser Ser Phe Ser Leu Ser Ser Thr Glu Val His Met Val
130 135 140

Arg Pro Gly Tyr Ser His Arg Val Ser Leu Pro Thr Ser Pro Gly Ile
145 150 155 160

Leu Ala Thr Ser Pro Tyr Pro Glu Thr Asp Ser Ala Phe Phe Glu Pro
165 170 175

Ser His Leu Thr Ser Ala Ala Asp Glu Gly Ala Val Gln Val Ser Arg
180 185 190

Arg Thr Ile Ser Ser Asn Ser Phe Ser Pro Glu Val Phe Val Leu Pro
195 200 205

Val Asp Val Glu Lys Glu Asn Ala His Phe Tyr Val Ala Asp Met Ile
210 215 220

Ile Ser Ala Met Glu Lys Met Lys Cys Asn Ile Leu Ser Gln Gln
225 230 235 240

Thr Glu Ser Trp Ser Lys Glu Val Ser Gly Leu Leu Gly Ser Asp Gln
 245 250 255
 Pro Asp Ser Glu Met Thr Phe Asp Thr Asn Ile Lys Gln Glu Ser Gly
 260 265 270
 Ser Ser Thr Ser Ser Tyr Ser Gly Tyr Glu Gly Cys Ala Val Leu Gln
 275 280 285
 Val Ser Pro Val Thr Glu Thr Arg Thr Tyr His Asp Val Lys Glu Ile
 290 295 300
 Cys Lys Cys Asp Val Asp Glu Phe Val Ile Leu Glu Leu Gly Asp Phe
 305 310 315 320
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 325 330 335
 Val Thr Tyr Glu Pro Asp Phe Asn Ser Ala Glu Leu Leu Ala Lys Glu
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 Leu Tyr Arg Val Phe Gln Lys Cys Trp Ile Leu Ser Val Val Asn Ser
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 Gln Leu Ala Gly Ser Leu Ser Ala Ala Gly Ser Ile Val Val Asn Glu
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 Ile Lys Phe Lys Ser Arg Ile Arg Gly Thr Glu Asp Trp Ala Pro Pro
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 Glu Pro Lys Phe Val Lys Arg Leu Arg Tyr Cys Glu Tyr Leu Gly Lys
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 Tyr Phe Cys Asp Cys Cys His Ser Tyr Ala Glu Ser Cys Ile Pro Ala
 465 470 475 480
 Arg Ile Leu Met Met Trp Asp Phe Lys Lys Tyr Tyr Val Ser Asn Phe
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 Ser Lys Gln Leu Leu Asp Ser Ile Trp His Gln Pro Ile Phe Asn Leu
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 Val Lys Glu Ile Gln Glu Gln Leu Phe His Ile Lys Lys Leu Leu Lys
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 Ala Ser Leu Ala His Val Ala Gly Cys Glu Leu Cys Gln Gly Lys Gly
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 Phe Ile Cys Glu Phe Cys Gln Asn Thr Thr Val Ile Phe Pro Phe Gln
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 Thr Ala Thr Cys Arg Arg Cys Ser Ala Cys Arg Ala Cys Phe His Lys
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Leu Asn Thr Asp His Pro Pro Cys Gln Leu Asp Ile Arg Leu Met Arg
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His Lys Ala Val Trp Ile Asn Pro Gln Asp Val Gln Gln Gln Pro Gln
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Asp Leu Gln Ser Gln Val Pro Ala Ala Gly Asn Ser Gly Thr His Phe
 65 70 75 80

Val Thr Asp Ala Ala Ser Pro Ser Gly Pro Ser Pro Ser Cys Leu Gly
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Asp Ser Leu Ala Glu Thr Thr Leu Ser Glu Asp Thr Thr Asp Ser Val
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Gly Ser Ala Ser Pro His Gly Ser Ser Glu Lys Ser Ser Ser Phe Ser
 115 120 125

Leu Ser Ser Thr Glu Val His Met Val Arg Pro Gly Tyr Ser His Arg
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 Val Ser Leu Pro Thr Ser Pro Gly Ile Leu Ala Thr Ser Pro Tyr Pro
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 Asp Glu Gly Ala Val Gln Val Ser Arg Arg Thr Ile Ser Ser Asn Ser
 180 185 190
 Phe Ser Pro Glu Val Phe Val Leu Pro Val Asp Val Glu Lys Glu Asn
 195 200 205
 Ala His Phe Tyr Val Ala Asp Met Ile Ile Ser Ala Met Glu Lys Met
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 Lys Cys Asn Ile Leu Ser Gln Gln Gln Thr Glu Ser Trp Ser Lys Glu
 225 230 235 240
 Val Ser Gly Leu Leu Gly Ser Asp Gln Pro Asp Ser Glu Met Thr Phe
 245 250 255
 Asp Thr Asn Ile Lys Gln Glu Ser Gly Ser Ser Thr Ser Ser Tyr Ser
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 Gly Tyr Glu Gly Cys Ala Val Leu Gln Val Ser Pro Val Thr Glu Thr
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 385 390 395 400
 Arg Gly Thr Glu Asp Trp Ala Pro Pro Arg Phe Gln Ile Ile Phe Asn
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 Asn Thr Thr Val Ile Phe Pro Phe Gln Thr Ala Thr Cys Arg Arg Cys
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Leu Asn Thr Asp His Pro Pro Cys Gln Leu Asp Ile Arg Leu Met Arg
35 40 45

His Lys Ala Val Trp Ile Asn Pro Gln Asp Val Gln Gln Gln Pro Gln
50 55 60

Asp Leu Gln Ser Gln Val Pro Ala Ala Gly Asn Ser Gly Thr His Phe
65 70 75 80

Val Thr Asp Ala Ala Ser Pro Ser Gly Pro Ser Pro Ser Cys Leu Gly
85 90 95

Asp Ser Leu Ala Glu Thr Thr Leu Ser Glu Asp Thr Thr Asp Ser Val
100 105 110

Gly Ser Ala Ser Pro His Gly Ser Ser Glu Lys Ser Ser Ser Phe Ser
115 120 125

Leu Ser Ser Thr Glu Val His Met Val Arg Pro Gly Tyr Ser His Arg
 130 135 140
 Val Ser Leu Pro Thr Ser Pro Gly Ile Leu Ala Thr Ser Pro Tyr Pro
 145 150 155 160
 Glu Thr Asp Ser Ala Phe Phe Glu Pro Ser His Leu Thr Ser Ala Ala
 165 170 175
 Asp Glu Gly Ala Val Gln Val Ser Arg Arg Thr Ile Ser Ser Asn Ser
 180 185 190
 Phe Ser Pro Glu Val Phe Val Leu Pro Val Asp Val Glu Lys Glu Asn
 195 200 205
 Ala His Phe Tyr Val Ala Asp Met Ile Ile Ser Ala Met Glu Lys Met
 210 215 220
 Lys Cys Asn Ile Leu Ser Gln Gln Gln Thr Glu Ser Trp Ser Lys Glu
 225 230 235 240
 Val Ser Gly Leu Leu Gly Ser Asp Gln Pro Asp Ser Glu Met Thr Phe
 245 250 255
 Asp Thr Asn Ile Lys Gln Glu Ser Gly Ser Ser Thr Ser Ser Tyr Ser
 260 265 270
 Gly Tyr Glu Gly Cys Ala Val Leu Gln Val Ser Pro Val Thr Glu Thr
 275 280 285
 Arg Thr Tyr His Asp Val Lys Glu Ile Cys Lys Cys Asp Val Asp Glu
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 Phe Val Ile Leu Glu Leu Gly Asp Phe Asn Asp Ile Thr Glu Thr Cys
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 Asn Ser Ala Glu Leu Leu Ala Lys Glu Leu Tyr Arg Val Phe Gln Lys
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 Cys Trp Ile Leu Ser Val Val Asn Ser Gln Leu Ala Gly Ser Leu Ser
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 Ala Ala Gly Ser Ile Val Val Asn Glu Glu Cys Val Arg Lys Asp Phe
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 Arg Gly Thr Glu Asp Trp Ala Pro Pro Arg Phe Gln Ile Ile Phe Asn
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 Tyr Ala Lys Ala Lys Glu Leu Asp Arg Val Lys Glu Ile Gln Glu Gln
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<212> PRT
<213> Homo sapiens

<400> 15
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Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly
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Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
35 40 45

Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
50 55 60

Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
65 70 75 80

Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
85 90 95

Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
100 105 110

Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
115 120 125

Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
130 135 140

Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
145 150 155 160

His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
165 170 175

Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
180 185 190

Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
195 200 205

Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
210 215 220

Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
225 230 235 240

Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
245 250 255

Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
260 265 270

Glu Ile Phe Cys Pro Ser Pro Pro Pro Ile Leu Asn Gly Arg His Ile
 275 280 285
 Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr
 290 295 300
 Cys Asp Pro Asp Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu
 305 310 315 320
 Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser
 325 330 335
 Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro
 340 345 350
 His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg
 355 360 365
 Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr
 370 375 380
 Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu
 385 390 395 400
 Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile
 405 410 415
 Leu Asn Gly Gln Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly
 420 425 430
 Thr Ser Ile Lys Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu
 435 440 445
 Glu Ser Ile Gln Cys Thr Ser Glu Gly Val Trp Thr Pro Pro Val Pro
 450 455 460
 Gln Cys Lys Val Ala Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr
 465 470 475 480
 Lys Pro Gln His Gln Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly
 485 490 495
 Glu Gly Tyr Lys Leu Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr
 500 505 510
 Ile Pro Trp Phe Met Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro
 515 520 525
 Pro Pro Pro Val Ile Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu
 530 535 540
 Asp Phe Pro Tyr Gly Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro
 545 550 555 560
 Glu Arg Gly Val Glu Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys
 565 570 575
 Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu
 580 585 590

Cys Lys Leu Ser Leu Leu Ala Val Gln Cys Ser His Val His Ile Ala
 595 600 605
 Asn Gly Tyr Lys Ile Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp
 610 615 620
 Thr Val Thr Phe Lys Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser
 625 630 635 640
 Gln Ile Arg Cys Lys Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val
 645 650 655
 Cys Glu Lys Glu Thr Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu
 660 665 670
 Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly
 675 680 685
 Tyr Gln Leu Thr Gly His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn
 690 695 700
 Gly Ile Trp Phe Lys Lys Ile Pro Leu Cys Lys Val Ile His Cys His
 705 710 715 720
 Pro Pro Pro Val Ile Val Asn Gly Lys His Thr Gly Met Met Ala Glu
 725 730 735
 Asn Phe Leu Tyr Gly Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe
 740 745 750
 Tyr Leu Leu Gly Glu Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly
 755 760 765
 His Gly Ser Trp Ser Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro
 770 775 780
 Val Thr Arg Cys Pro Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn
 785 790 795 800
 Lys Thr His Ser Ala Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys
 805 810 815
 Asn Pro Gly Phe Ile Met Asn Gly Ser Arg Val Ile Arg Cys His Thr
 820 825 830
 Asp Asn Thr Trp Val Pro Gly Val Pro Thr Cys Met Lys Lys Ala Phe
 835 840 845
 Ile Gly Cys Pro Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly
 850 855 860
 Gly Asn Ile Ala Arg Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys
 865 870 875 880
 Asp Gln Gly Tyr Leu Leu Val Gly Glu Ala Leu Leu Cys Thr His
 885 890 895
 Glu Gly Thr Trp Ser Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys
 900 905 910

Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg
915 920 925

Lys Met Tyr Gln Tyr Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly
930 935 940

Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln
945 950 955 960

Trp Asn Pro Pro Leu Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val
965 970 975

Leu Cys Gly Ile Ala Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val
980 985 990

Ile Thr Leu Tyr Val Ile Ser Lys His Arg Glu Arg Asn Tyr Tyr Thr
995 1000 1005

Asp Thr Ser Gln Lys Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr
1010 1015 1020

Ser Val Asp Pro Tyr Asn Pro Ala Ser
1025 1030

<210> 16
<211> 637
<212> DNA
<213> Homo sapiens

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cagagggcct tccttgagaa ctgtggggaa ggaggccctg ggggtttctt ctgttaggcag 180
agctcaggcc ccagtcacct ctgccaccct cagcctggca ctgttgtgcc agaggctctg 240
ctgcctctct cttcctaccc atctgcagac cagcagaata ttctccccct ctcatcacca 300
accaggagtt tgggtgtggtt tctggacacg gccagagcag tcactgcggg gctggtttg 360
ctgggcttcc ctgtcaaagc aatgctaacg tccagctctc gactcaaggg caggttcttc 420
tcccacttgt ggcctcttgg gcttggaggc tgagccaggg gctcctctcc tgctggccgt 480
ccaggaacag acatcttac atccctagtc ttccaaaccc ggaccatgcc gtcttgactc 540
ccggtgatga tggatctggct tggatctccat gctggggccct ccatcaggca gcaacagggtt 600
atggctcctt ctggggccca ggctgtggtg atgctgg 637

<210> 17
<211> 4191
<212> DNA
<213> Homo sapiens

<400> 17
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gaggtgatgc agcgatgtc agagacggca aagagctca gccaagtgcga gaagctgctg 120
ctgccccttc tcttgccaac atctcctgt tcacccagaa gctgggtggag aagctgtaca 180
gtggatgtt ctcggcagac cccaggcata tcctcctt catcctggag cacatcatgg 240
tggatgttga gactgcctt tctcaaaggg acactgtcct cagcacttta tacagcagtt 300
taaataaaagt catttttat tgcctatcca agccccagca gtcctctcc gaatgcctcg 360

gccttctcag catcctggc tttctgcagg agcaactgggta tggtgtctt gccacccata 420
 attccaacat cagcttcctc ctgtgtctca tgcattgcct tttgtactc aatgagagaa 480
 gttaccaga aggatttggg ttggagccca agcctagaat gtctacttat catcaagtct 540
 tccttccccaa aaatgaagac gtgaaagaaa aaagagaaga cttaccaagt ttgagtgtg 600
 tccaaacacaa catccagaag acatgcaga ctctctggca gcagctggg gcacaaaggc 660
 agcagaccct ggaggatgcc ttcaagatcg atctctctgt gaaacctgga gagagggaaag 720
 tgaagattga agaggtcaca ccgtctggg aggagacat gtcaggcc tggcagcatt 780
 acttagcatc tgagaagaag tcaactggcaa gtcgttcaaa tggtgcacac cacagcaaag 840
 tcactttgtg gagtggaaagc ctgtcttcag ccatgaagct gatgcccggg cggcaggcca 900
 aggaccctga gtcaagaca gaggattttg tgcattgtat agagaactac agaagaagag 960
 gacaagagct atatgcattt ttatacaacaa accatgtgca aaggcgaaaaa tggcaaca 1020
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 aacattctca catctgcgag aacttcacac tgcattttcac gggtgatgtc tactgtaccc 1560
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 gagagggaccc ctcggctca gtcctcaagcc caagggcca caagtgggag aagaacctgg 3660
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 ccgcagtgcac tgcattttt gtttgcaccc accacacca actcctgttt ggtgatgaga 3780
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<211> 1606
<212> PRT
<213> Homo sapiens

<400> 18
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Asn Cys Ala Gly His Leu Ser Gly Ser Leu Arg Thr Ile Gly Ala Val
20 25 30

Ala Val Gly Gln Leu Gly Val Arg Val Phe His Ser Ser Pro Ala Ala
35 40 45

Ser Ser Leu Asp Phe Ile Gly Gly Pro Ala Ile Leu Leu Gly Leu Ile
50 55 60

Ser Leu Ala Thr Asp Asp His Thr Met Tyr Ala Ala Val Lys Val Leu
65 70 75 80

His Ser Val Leu Thr Ser Asn Ala Met Cys Asp Phe Leu Met Gln His
85 90 95

Ile Cys Gly Tyr Gln Ile Met Ala Phe Leu Leu Arg Lys Lys Ala Ser
100 105 110

Leu Leu Asn His Arg Ile Phe Gln Leu Ile Leu Ser Val Ala Gly Thr
115 120 125

Val Glu Leu Gly Phe Arg Ser Ser Ala Ile Thr Asn Thr Gly Val Phe
130 135 140

Gln His Ile Leu Cys Asn Phe Glu Leu Trp Met Asn Thr Ala Asp Asn
145 150 155 160

Leu Glu Leu Ser Leu Phe Ser His Leu Leu Glu Ile Leu Gln Ser Pro
165 170 175

Arg Glu Gly Pro Arg Asn Ala Glu Ala Ala His Gln Ala Gln Leu Ile
180 185 190

Pro Lys Leu Ile Phe Leu Phe Asn Glu Pro Ser Leu Ile Pro Ser Lys
195 200 205

Ile Pro Thr Ile Ile Gly Ile Leu Ala Cys Gln Leu Arg Gly His Phe
210 215 220

Ser Thr Gln Asp Leu Leu Arg Ile Gly Leu Phe Val Val Tyr Thr Leu
225 230 235 240

Lys Pro Ser Ser Val Asn Glu Arg Gln Ile Cys Met Asp Gly Ala Leu
245 250 255

Asp Pro Ser Leu Pro Ala Gly Ser Gln Thr Ser Gly Lys Thr Ile Trp
260 265 270

Leu Arg Asn Gln Leu Leu Glu Met Leu Leu Ser Val Ile Ser Ser Pro
 275 280 285
 Gln Leu His Leu Ser Ser Glu Ser Lys Glu Glu Met Phe Leu Lys Leu
 290 295 300
 Gly Pro Asp Trp Phe Leu Leu Leu Gln Gly His Leu His Ala Ser
 305 310 315 320
 Thr Thr Val Leu Ala Leu Lys Leu Leu Tyr Phe Leu Ala Ser Pro
 325 330 335
 Ser Leu Arg Thr Arg Phe Arg Asp Gly Leu Cys Ala Gly Ser Trp Val
 340 345 350
 Glu Arg Ser Thr Glu Gly Val Asp Ile Val Met Asp Asn Leu Lys Ser
 355 360 365
 Gln Ser Pro Leu Pro Glu Gln Ser Pro Cys Leu Leu Pro Gly Phe Arg
 370 375 380
 Val Leu Asn Asp Phe Leu Ala His His Val His Ile Pro Glu Val Tyr
 385 390 395 400
 Leu Ile Val Ser Thr Phe Phe Leu Gln Thr Pro Leu Thr Glu Leu Met
 405 410 415
 Asp Gly Pro Lys Asp Ser Leu Asp Ala Met Leu Gln Trp Leu Leu Gln
 420 425 430
 Arg His His Gln Glu Glu Val Leu Gln Ala Gly Leu Cys Thr Glu Gly
 435 440 445
 Ala Leu Leu Leu Leu Glu Met Leu Lys Ala Thr Met Ser Gln Pro Leu
 450 455 460
 Ala Gly Ser Glu Asp Gly Ala Trp Ala Gln Thr Phe Pro Ala Ser Val
 465 470 475 480
 Leu Gln Phe Leu Ser Leu Val His Arg Thr Tyr Pro Gln Asp Pro Ala
 485 490 495
 Trp Arg Ala Pro Glu Phe Leu Gln Thr Leu Ala Ile Ala Ala Phe Pro
 500 505 510
 Leu Gly Ala Gln Lys Gly Val Gly Ala Glu Ser Thr Arg Asn Thr Ser
 515 520 525
 Ser Pro Glu Ala Ala Ala Glu Gly Asp Ser Thr Val Glu Gly Leu Gln
 530 535 540
 Ala Pro Thr Lys Ala His Pro Ala Arg Arg Lys Leu Arg Glu Phe Thr
 545 550 555 560
 Gln Leu Leu Leu Arg Glu Leu Leu Gly Ala Ser Ser Pro Lys Gln
 565 570 575
 Trp Leu Pro Leu Glu Val Leu Leu Glu Ala Ser Pro Asp His Ala Thr
 580 585 590

Ser Gln Gln Lys Arg Asp Phe Gln Ser Glu Val Leu Leu Ser Ala Met
 595 600 605
 Glu Leu Phe His Met Thr Ser Gly Gly Asp Ala Ala Met Phe Arg Asp
 610 615 620
 Gly Lys Glu Pro Gln Pro Ser Ala Glu Ala Ala Ala Pro Ser Leu
 625 630 635 640
 Ala Asn Ile Ser Cys Phe Thr Gln Lys Leu Val Glu Lys Leu Tyr Ser
 645 650 655
 Gly Met Phe Ser Ala Asp Pro Arg His Ile Leu Leu Phe Ile Leu Glu
 660 665 670
 His Ile Met Val Val Ile Glu Thr Ala Ser Ser Gln Arg Asp Thr Val
 675 680 685
 Leu Ser Thr Leu Tyr Ser Ser Leu Asn Lys Val Ile Leu Tyr Cys Leu
 690 695 700
 Ser Lys Pro Gln Gln Ser Leu Ser Glu Cys Leu Gly Leu Leu Ser Ile
 705 710 715 720
 Leu Gly Phe Leu Gln Glu His Trp Asp Val Val Phe Ala Thr Tyr Asn
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 Ser Asn Ile Ser Phe Leu Leu Cys Leu Met His Cys Leu Leu Leu
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 Asn Glu Arg Ser Tyr Pro Glu Gly Phe Gly Leu Glu Pro Lys Pro Arg
 755 760 765
 Met Ser Thr Tyr His Gln Val Phe Leu Ser Pro Asn Glu Asp Val Lys
 770 775 780
 Glu Lys Arg Glu Asp Leu Pro Ser Leu Ser Asp Val Gln His Asn Ile
 785 790 795 800
 Gln Lys Thr Val Gln Thr Leu Trp Gln Gln Leu Val Ala Gln Arg Gln
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 Gln Thr Leu Glu Asp Ala Phe Lys Ile Asp Leu Ser Val Lys Pro Gly
 820 825 830
 Glu Arg Glu Val Lys Ile Glu Glu Val Thr Pro Leu Trp Glu Glu Thr
 835 840 845
 Met Leu Lys Ala Trp Gln His Tyr Leu Ala Ser Glu Lys Lys Ser Leu
 850 855 860
 Ala Ser Arg Ser Asn Val Ala His His Ser Lys Val Thr Leu Trp Ser
 865 870 875 880
 Gly Ser Leu Ser Ser Ala Met Lys Leu Met Pro Gly Arg Gln Ala Lys
 885 890 895
 Asp Pro Glu Cys Lys Thr Glu Asp Phe Val Ser Cys Ile Glu Asn Tyr
 900 905 910

Arg Arg Arg Gly Gln Glu Leu Tyr Ala Ser Leu Tyr Lys Asp His Val
 915 920 925

Gln Arg Arg Lys Cys Gly Asn Ile Lys Ala Ala Asn Ala Trp Ala Arg
 930 935 940

Ile Gln Glu Gln Leu Phe Gly Glu Leu Gly Leu Trp Ser Gln Gly Glu
 945 950 955 960

Glu Thr Lys Pro Cys Ser Pro Trp Glu Leu Asp Trp Arg Glu Gly Pro
 965 970 975

Ala Arg Met Arg Lys Arg Ile Lys Arg Leu Ser Pro Leu Glu Ala Leu
 980 985 990

Ser Ser Gly Arg His Lys Glu Ser Gln Asp Lys Asn Asp His Ile Ser
 995 1000 1005

Gln Thr Asn Ala Glu Asn Gln Asp Glu Leu Thr Leu Arg Glu Ala Glu
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Gly Glu Pro Asp Glu Val Gly Val Asp Cys Thr Gln Leu Thr Phe Phe
 1025 1030 1035 1040

Pro Ala Leu His Glu Ser Leu His Ser Glu Asp Phe Leu Glu Leu Cys
 1045 1050 1055

Arg Glu Arg Gln Val Ile Leu Gln Glu Leu Leu Asp Lys Glu Lys Val
 1060 1065 1070

Thr Gln Lys Phe Ser Leu Val Ile Val Gln Gly His Leu Val Ser Glu
 1075 1080 1085

Gly Val Leu Leu Phe Gly His Gln His Phe Tyr Ile Cys Glu Asn Phe
 1090 1095 1100

Thr Leu Ser Pro Thr Gly Asp Val Tyr Cys Thr Arg His Cys Leu Ser
 1105 1110 1115 1120

Asn Ile Ser Asp Pro Phe Ile Phe Asn Leu Cys Ser Lys Asp Arg Ser
 1125 1130 1135

Thr Asp His Tyr Ser Cys Gln Cys His Ser Tyr Ala Asp Met Arg Glu
 1140 1145 1150

Leu Arg Gln Ala Arg Phe Leu Leu Gln Asp Ile Ala Leu Glu Ile Phe
 1155 1160 1165

Phe His Asn Gly Tyr Ser Lys Phe Leu Val Phe Tyr Asn Asn Asp Arg
 1170 1175 1180

Ser Lys Ala Phe Lys Ser Phe Cys Ser Phe Gln Pro Ser Leu Lys Gly
 1185 1190 1195 1200

Lys Ala Thr Ser Glu Asp Thr Leu Asn Leu Arg Arg Tyr Pro Gly Ser
 1205 1210 1215

Asp Arg Ile Met Leu Gln Lys Trp Gln Lys Arg Asp Ile Ser Asn Phe
 1220 1225 1230

Glu Tyr Leu Met Tyr Leu Asn Thr Ala Ala Gly Arg Thr Cys Asn Asp
 1235 1240 1245
 Tyr Met Gln Tyr Pro Val Phe Pro Trp Val Leu Ala Asp Tyr Thr Ser
 1250 1255 1260
 Glu Thr Leu Asn Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys
 1265 1270 1275 1280
 Pro Met Gly Ala Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg
 1285 1290 1295
 Phe Lys Glu Val Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His
 1300 1305 1310
 Tyr Tyr Thr His Tyr Ser Ser Ala Ile Ile Val Ala Ser Tyr Leu Val
 1315 1320 1325
 Arg Met Pro Pro Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Gly Ser
 1330 1335 1340
 Phe Asp Val Ala Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu
 1345 1350 1355 1360
 Ser Ala Ser Arg Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu
 1365 1370 1375
 Phe Phe Tyr Leu Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe
 1380 1385 1390
 Gly Cys Met Gln Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro
 1395 1400 1405
 Trp Ala Asp Gly Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala
 1410 1415 1420
 Leu Glu Ser Asp Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu
 1425 1430 1435 1440
 Ile Phe Gly Tyr Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn
 1445 1450 1455
 Ile Phe His Pro Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile
 1460 1465 1470
 Thr Asp Pro Leu Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe
 1475 1480 1485
 Gly Gln Val Pro Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr
 1490 1495 1500
 Ala Ala Gly Lys Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser
 1505 1510 1515 1520
 Leu Pro Gly His Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg
 1525 1530 1535
 Pro Ser Gln Val Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser
 1540 1545 1550

Glu Ser Pro Lys Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr
1555 1560 1565

Ile Leu Ala Val Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn
1570 1575 1580

Arg Thr Phe Ser Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser
1585 1590 1595 1600

Tyr Gly Ser Asp Lys Ser
1605

<210> 19

<211> 426

<212> DNA

<213> Homo sapiens

<400> 19

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ggcgtggac acctgcaact ccatccttag ctttgtcacc tcctccggaa gtctttccag 180
caaatctgaa gttcgttcc tctcgtaa ttccgtggac ttgaagctgc tcagatctgc 240
ttgaagcccg ttcaagggtcc aggacagctc caagtctga gatttcaatc tctgtgttc 300
agctcgaagt tcctccaggat cctgtgaaat ctgcgtggac tgggatttc gcgcctctg 360
gtcaccgtgg tggcttcca agttcttggaa aacttgagag acgttccggg cagccctctc 420
ttccag 426

<210> 20

<211> 1569

<212> DNA

<213> Homo sapiens

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Ser Gln Val Ser Lys Asn Leu Glu Ser His His Gly Asp Gln Met Ala
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Ala Glu Gln Gln Arg Leu Lys Ser Gln Asp Leu Glu Leu Ser Trp Asn
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Val Thr Lys Leu Arg Met Glu Leu Gln Val Ser Ser Gly Phe Val Cys
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245 250 255

Glu Asp Cys Val Met Met Arg Gly Ser Gly Arg Trp Asn Asp Ala Phe
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Cys Asp Arg Lys Leu Gly Ala Trp Val Cys Asp Arg Leu Ala Thr Cys
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Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro
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Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys
 35 40 45

Ser Asp Arg Gly Met Ala Ser Asn Val Lys Val Glu Thr Gln Ser Asp
 50 55 60

Glu Glu Asn Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu
 65 70 75 80

Asp Leu Arg Met Leu Asp Ala Ser Gly Glu Lys Met Asn Gly Ser His
 85 90 95

Arg Asp Gln Gly Ser Ser Ala Leu Ser Gly Val Gly Gly Ile Arg Leu
 100 105 110

Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Val Cys Ile Gly
 115 120 125

Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro
 130 135 140

Phe Gln Cys Asn Gln Cys Ser Ser Ala Leu Ser Gly Val Gly Gly Ile
 145 150 155 160

Arg Leu Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Val Cys
 165 170 175

Ile Gly Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu
 180 185 190

Arg Pro Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly
 195 200 205

Asn Leu Leu Arg His Ile Lys Leu His Ser Gly Glu Lys Pro Phe Lys
 210 215 220

Cys His Leu Cys Asn Tyr Ala Cys Arg Arg Asp Ala Leu Thr Gly
 225 230 235 240

His Leu Arg Thr His Ser Val Gly Lys Pro His Lys Cys Gly Tyr Cys
 245 250 255

Gly Arg Ser Tyr Lys Gln Arg Ser Ser Leu Glu Glu His Lys Glu Arg
 260 265 270

Cys His Asn Tyr Leu Glu Ser Met Gly Leu Pro Gly Met Tyr Pro Val
 275 280 285

Ile Lys Glu Glu Thr Asn His Asn Glu Met Ala Glu Asp Leu Cys Lys
 290 295 300

Ile Gly Ala Glu Arg Ser Leu Val Leu Asp Arg Leu Ala Ser Asn Val
 305 310 315 320

Ala Lys Arg Lys Ser Ser Met Pro Gln Lys Phe Leu Gly Asp Lys Cys
 325 330 335

Leu Ser Asp Met Pro Tyr Asp Ser Ala Asn Tyr Glu Lys Glu Asp Met
 340 345 350

Met Thr Ser His Val Met Asp Gln Ala Ile Asn Asn Ala Ile Asn Tyr
 355 360 365

Leu Gly Ala Glu Ser Leu Arg Pro Leu Val Gln Thr Pro Pro Gly Ser
 370 375 380

Ser Glu Val Val Pro Val Ile Ser Ser Met Tyr Gln Leu His Lys Pro
 385 390 395 400

Pro Ser Asp Gly Pro Pro Arg Ser Asn His Ser Ala Gln Asp Ala Val
 405 410 415

Asp Asn Leu Leu Leu Ser Lys Ala Lys Ser Val Ser Ser Glu Arg
 420 425 430

Glu Ala Ser Pro Ser Asn Ser Cys Gln Asp Ser Thr Asp Thr Glu Ser
 435 440 445

Asn Ala Glu Glu Gln Arg Ser Gly Leu Ile Tyr Leu Thr Asn His Ile
 450 455 460

Asn Pro His Ala Arg Asn Gly Leu Ala Leu Lys Glu Glu Gln Arg Ala
 465 470 475 480

Tyr Glu Val Leu Arg Ala Ala Ser Glu Asn Ser Gln Asp Ala Phe Arg
 485 490 495

Val Val Ser Thr Ser Gly Glu Gln Leu Lys Val Tyr Lys Cys Glu His
 500 505 510

Cys Arg Val Leu Phe Leu Asp His Val Met Tyr Thr Ile His Met Gly
 515 520 525

Cys His Gly Cys His Gly Phe Arg Asp Pro Phe Glu Cys Asn Met Cys
 530 535 540

Gly Tyr His Ser Gln Asp Arg Tyr Glu Phe Ser Ser His Ile Thr Arg
 545 550 555 560

Gly Glu His Arg Tyr His Leu Ser
 565

<210> 27
 <211> 350
 <212> DNA
 <213> Homo sapiens

<400> 27
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 ttttttaac ttttgtctt gagataattt tagatttaca gaagagttgc aaaaagagta 180
 gagagagttc ctgtacaccc ttccaccagc ttccctctact gctaacatct tacataatca 240
 tagttcaac ctgagaaattt agcatgggtt acagtcctat taatgaaacc ccaggctta 300
 ttcagatttc accaggtttt cagtaacatc ctttatctgt ttcagaattt 350

<210> 28
 <211> 850
 <212> DNA
 <213> Homo sapiens

<400> 28

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gcgcttattt ttcttaatca ttttctgac aatcatagtg tgtggatgg ttgctgctt 180
aagcgcata agagctaact gccatcaaga gccatcaga tgcattcaag ctgcattgccc 240
agaaagctgg attggtttc aaagaaagtg tttctatTTT tctgatgaca ccaagaactg 300
gacatcaagt cagaggTTT gtgactcaca agatgctgat cttgctcagg ttgaaagctt 360
ccaggaactg aatttcctgt tgagatataa aggccatct gatcaactgga ttggctgag 420
cagagaacaa ggccaaccat ggaatggat aaatggact gaatggacaa gacagttcc 480
tatcctggg gcaggagagt gtcctattt gaatgacaaa ggtgccagta gtgcaggca 540
ctacacagag aggaagtgga ttgttccaa atcagatata catgtctaga tgtagacca 600
aagccccaaac taatcttttag aagcatattg gaaactgataa ctccatTTT aaatgagcaa 660
agaatttatt tcttatacca acaggtatat gaaaatatgc tcaatatcac taataactgg 720
gaaaatacaa atcaaaaatca tagtaaaata ttacctgtt tcacggctgct aatattacct 780
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ttgaaaaaaaaa 850

<210> 29

<211> 191

<212> PRT

<213> Homo sapiens

<400> 29

Met His Asp Ser Asn Asn Val Glu Lys Asp Ile Thr Pro Ser Glu Leu
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Pro Ala Asn Pro Gly Cys Leu His Ser Lys Glu His Ser Ile Lys Ala
20 25 30

Thr Leu Ile Trp Arg Leu Phe Phe Leu Ile Met Phe Leu Thr Ile Ile
35 40 45

Val Cys Gly Met Val Ala Ala Leu Ser Ala Ile Arg Ala Asn Cys His
50 55 60

Gln Glu Pro Ser Val Cys Leu Gln Ala Ala Cys Pro Glu Ser Trp Ile
65 70 75 80

Gly Phe Gln Arg Lys Cys Phe Tyr Phe Ser Asp Asp Thr Lys Asn Trp
85 90 95

Thr Ser Ser Gln Arg Phe Cys Asp Ser Gln Asp Ala Asp Leu Ala Gln
100 105 110

Val Glu Ser Phe Gln Glu Leu Asn Phe Leu Leu Arg Tyr Lys Gly Pro
115 120 125

Ser Asp His Trp Ile Gly Leu Ser Arg Glu Gln Gly Gln Pro Trp Lys
130 135 140

Trp Ile Asn Gly Thr Glu Trp Thr Arg Gln Phe Pro Ile Leu Gly Ala
145 150 155 160

Gly Glu Cys Ala Tyr Leu Asn Asp Lys Gly Ala Ser Ser Ala Arg His
165 170 175

Tyr Thr Glu Arg Lys Trp Ile Cys Ser Lys Ser Asp Ile His Val
180 185 190

<210> 30
<211> 558
<212> DNA
<213> Homo sapiens

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<223> n = g, a, c or t

<400> 30

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tgggtttgc atccagggtt ccagcaggat ctcttcagt gagggtcgaa aagaagggtt 180
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gtcatagagg agatgccc gtgaccagac agtggccggg agtgcattgt actggtgtcg 360
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tggctgccac tactttgg 558

<210> 31
<211> 2088
<212> DNA
<213> Homo sapiens

<400> 31

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cccgccgtc cacgccttcgccc gggcttagcg gggtcaatctg cgcagcgcga 180
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cgccaggagg caaggatcggtt gaagcgttcg aggccgaga tegactcgcc cccctccctgg 300
gtaagggggg ctttggcacc gtcttcgcag gacaccgcctt cacatcgatca ctccaggtgg 360
ccatcaaagt gattccccgg aatcgtgtc tgggctggc ccccttgcata gactcagtca 420
catgcccact cgaagtcgca ctgttatggaa aagtgggtgc aggtgggtggg caccctggcg 480
tgatccgcct gcttgcgttggg tttgagacac aggaaggctt catgtctggc ctcgagcggc 540
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caagccgtc cttctttggc caagtagtgg cagccatcca gcaactgcctt tcccgtggag 660
ttgtccatcg tgacatcaag gatgagaaca tcctgtataga cttacgcgcgtt ggctgtggca 720
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.ccactatcca ataaaagtaa tagaatcaga aaaaaaaaaa aaaaaaaaa 2088

<210> 32
<211> 334
<212> PRT
<213> Homo sapiens

<400> 32
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Thr Pro Pro Pro Gly Gly Lys Asp Arg Glu Ala Phe Glu Ala Glu Tyr
20 25 30

Arg Leu Gly Pro Leu Leu Gly Lys Gly Gly Phe Gly Thr Val Phe Ala
35 40 45

Gly His Arg Leu Thr Asp Arg Leu Gln Val Ala Ile Lys Val Ile Pro
50 55 60

Arg Asn Arg Val Leu Gly Trp Ser Pro Leu Ser Asp Ser Val Thr Cys
65 70 75 80

Pro Leu Glu Val Ala Leu Leu Trp Lys Val Gly Ala Gly Gly His
85 90 95

Pro Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Thr Gln Glu Gly Phe
100 105 110

Met Leu Val Leu Glu Arg Pro Leu Pro Ala Gln Asp Leu Phe Asp Tyr
115 120 125

Ile Thr Glu Lys Gly Pro Leu Gly Glu Gly Pro Ser Arg Cys Phe Phe
130 135 140

Gly Gln Val Val Ala Ala Ile Gln His Cys His Ser Arg Gly Val Val
145 150 155 160

His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Arg Arg Gly
165 170 175

Cys Ala Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu His Asp Glu
180 185 190

Pro Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp
195 200 205

Ile Ser Arg His Gln Tyr His Ala Leu Pro Ala Thr Val Trp Ser Leu
210 215 220

Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile Pro Phe Glu Arg
225 230 235 240

Asp Gln Glu Ile Leu Glu Ala Glu Leu His Phe Pro Ala His Val Ser
245 250 255

Pro Asp Cys Cys Ala Leu Ile Arg Arg Cys Leu Ala Pro Lys Pro Ser
260 265 270

Ser Arg Pro Ser Leu Glu Glu Ile Leu Leu Asp Pro Trp Met Gln Thr
275 280 285

Pro Ala Glu Asp Val Thr Pro Gln Pro Leu Gln Arg Arg Pro Cys Pro
290 295 300

Phe Gly Leu Val Leu Ala Thr Leu Ser Leu Ala Trp Pro Gly Leu Ala
305 310 315 320

Pro Asn Gly Gln Lys Ser His Pro Met Ala Met Ser Gln Gly
325 330

<210> 33

<211> 1215

<212> DNA

<213> Homo sapiens

<400> 33

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gactataaaac aaaatataatg taataggtgg tggtaagtac cgtggagaag taacaaaatgg 180
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ctcgtgggtgg tttcccttttgc tctccctttat tacatggggac tctgacatgtt gcccatacg 300
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aaaaaaaaaaaaaaa aaaaaa 1215

<210> 34

<211> 3144

<212> DNA

<213> Homo sapiens

<400> 34

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gagagctgac ggcctggggcc acccttcttc cttcaactggg caggcttga ggtgcttgc 180
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aagaaaactgc ttatccagct ttggaggaaa ccagctcaac aatttggggca gaggaacaaa 480
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atcagcccgat ccctgcctttt agacgacgccc gtcgttaggaa gaagaccgtt tctgcttcagc 780

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tgtacttcat	aataattttt	tatccatttt	catcttcttt	atctttatat	tctgtaaat	3060
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<210> 35
<211> 755
<212> PRT
<213> *Homo sapiens*

<400> 35
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Ile Ser His Glu Gly Ser Asp Ile Glu Met Leu Asn Ser Val Thr Pro
20 25 30

Thr Asp Ser Cys Glu Pro Ala Pro Glu Cys Ser Ser Leu Glu Gln Glu
35 40 45

Glu Leu Gln Ala Leu Gln Ile Glu Gln Gly Glu Ser Ser Gln Asn Gly
50 55 60

Thr Val Leu Met Glu Glu Thr Ala Tyr Pro Ala Leu Glu Glu Thr Ser
 65 70 75 80
 Ser Thr Ile Glu Ala Glu Glu Gln Lys Ile Pro Glu Asp Ser Ile Tyr
 85 90 95
 Ile Gly Thr Ala Ser Asp Asp Ser Asp Ile Val Thr Leu Glu Pro Pro
 100 105 110
 Lys Leu Glu Glu Ile Gly Asn Gln Glu Val Val Ile Val Glu Glu Ala
 115 120 125
 Gln Ser Ser Glu Asp Phe Asn Met Gly Ser Ser Ser Ser Gln Tyr
 130 135 140
 Thr Phe Cys Gln Pro Glu Thr Val Phe Ser Ser Gln Pro Ser Asp Asp
 145 150 155 160
 Glu Ser Ser Ser Asp Glu Thr Ser Asn Gln Pro Ser Pro Ala Phe Arg
 165 170 175
 Arg Arg Arg Ala Arg Lys Lys Thr Val Ser Ala Ser Glu Ser Glu Asp
 180 185 190
 Arg Leu Val Ala Glu Gln Glu Thr Glu Pro Ser Lys Glu Leu Ser Lys
 195 200 205
 Arg Gln Phe Ser Ser Gly Leu Asn Lys Cys Val Ile Leu Ala Leu Val
 210 215 220
 Ile Ala Ile Ser Met Gly Phe Gly His Phe Tyr Gly Thr Ile Gln Ile
 225 230 235 240
 Gln Lys Arg Gln Gln Leu Val Arg Lys Ile His Glu Asp Glu Leu Asn
 245 250 255
 Asp Met Lys Asp Tyr Leu Ser Gln Cys Gln Gln Glu Glu Ser Phe
 260 265 270
 Ile Asp Tyr Lys Ser Leu Lys Glu Asn Leu Ala Arg Cys Trp Thr Leu
 275 280 285
 Thr Glu Ala Glu Lys Met Ser Phe Glu Thr Gln Lys Thr Asn Leu Ala
 290 295 300
 Thr Glu Asn Gln Tyr Leu Arg Val Ser Leu Glu Lys Glu Glu Lys Ala
 305 310 315 320
 Leu Ser Ser Leu Gln Glu Glu Leu Asn Lys Leu Arg Glu Gln Ile Arg
 325 330 335
 Ile Leu Glu Asp Lys Gly Thr Ser Thr Glu Leu Val Lys Glu Asn Gln
 340 345 350
 Lys Leu Lys Gln His Leu Glu Glu Lys Gln Lys Lys His Ser Phe
 355 360 365
 Leu Ser Gln Arg Glu Thr Leu Leu Thr Glu Ala Lys Met Leu Lys Arg
 370 375 380

Glu Leu Glu Arg Glu Arg Leu Val Thr Thr Ala Leu Arg Gly Glu Leu
 385 390 395 400
 Gln Gln Leu Ser Gly Ser Gln Leu His Gly Lys Ser Asp Ser Pro Asn
 405 410 415
 Val Tyr Thr Glu Lys Lys Glu Ile Ala Ile Leu Arg Glu Arg Leu Thr
 420 425 430
 Glu Leu Glu Arg Lys Leu Thr Phe Glu Gln Gln Arg Ser Asp Leu Trp
 435 440 445
 Glu Arg Leu Tyr Val Glu Ala Lys Asp Gln Asn Gly Lys Gln Gly Thr
 450 455 460
 Asp Gly Lys Lys Lys Gly Gly Arg Gly Ser His Arg Ala Lys Asn Lys
 465 470 475 480
 Ser Lys Glu Thr Phe Leu Gly Ser Val Lys Glu Thr Phe Asp Ala Met
 485 490 495
 Lys Asn Ser Thr Lys Glu Phe Val Arg His His Lys Glu Lys Ile Lys
 500 505 510
 Gln Ala Lys Glu Ala Val Lys Glu Asn Leu Lys Lys Phe Ser Asp Ser
 515 520 525
 Val Lys Ser Thr Phe Arg His Phe Lys Asp Thr Thr Lys Asn Ile Phe
 530 535 540
 Asp Glu Lys Gly Asn Lys Arg Phe Gly Ala Thr Lys Glu Ala Ala Glu
 545 550 555 560
 Lys Pro Arg Thr Val Phe Ser Asp Tyr Leu His Pro Gln Tyr Lys Ala
 565 570 575
 Pro Thr Glu Asn His Ser Arg Pro Tyr Tyr Ala Lys Arg Trp Lys Glu
 580 585 590
 Glu Lys Pro Val His Phe Lys Glu Phe Arg Lys Asn Thr Asn Ser Lys
 595 600 605
 Lys Cys Ser Pro Gly His Asp Cys Arg Glu Asn Ser His Ser Phe Arg
 610 615 620
 Lys Ala Cys Ser Gly Val Phe Asp Cys Ala Gln Gln Glu Ser Met Ser
 625 630 635 640
 Leu Phe Asn Thr Val Val Ile Pro Ile Arg Met Asp Glu Phe Arg Gln
 645 650 655
 Ile Ile Gln Arg Tyr Met Leu Lys Glu Leu Asp Thr Phe Cys Arg Trp
 660 665 670
 Asn Glu Leu Asp Gln Phe Ile Asn Lys Phe Phe Leu Asn Gly Val Phe
 675 680 685
 Ile His Asp Gln Lys Leu Phe Thr Asp Phe Val Asn Asp Val Lys Ile
 690 695 700

Ile Leu Gly Asn Met Lys Glu Tyr Glu Val Asp Asn Asp Gly Val Phe
705 710 715 720

Glu Lys Leu Asp Glu Tyr Ile Tyr Arg His Phe Phe Gly His Thr Phe
725 730 735

Ser Pro Pro Tyr Gly Pro Arg Ser Val Tyr Ile Lys Pro Cys His Tyr
740 745 750

Ser Ser Leu
755

<210> 36
<211> 558
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1)..(558)
<223> n = g, a, c or t

<400> 36
ccatggatg gctttctga ccattggggg ccaggccagg ccaggccagg cttagggcag 60
caaggaccag gccaaagggg caggcctcc tttggagggg ttgagggta catcctcgcc 120
tgggtttgc atccaggggt ccagcaggat ctcttcagt gagggtcggg aagaaggttt 180
gggggccagg cacccggcgga ttagggcaca gcaatcttgg gaaaaacatg ggcttggaa 240
gtggagctca gtttccagaa tctctggc cctctcaaag ggaatgtccc cacacaccat 300
gtcatagagg aggtgtccca gtgaccagac agtggccggg agtgcatggt actgggtgtcg 360
agagatccac tctggggggc tgtacaccct tgtcccatca aagtcaagtgt agggttcatc 420
atgaagcagg gcaccagaac caaaatcaat gagtttgca cagccacggc gttaggtctat 480
caggatgntc tcataccttga tgtcacgatg gacaactnca cgggaaatgg cagtgctgga 540
tggctgccac tactttgg 558

<210> 37
<211> 86
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (1)..(86)
<223> Xaa = any amino acid

<400> 37
Gln Val Val Ala Xaa Ile Gln His Cys His Ser Arg Gly Val Val His
1 5 10 15

Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Arg Arg Gly Cys
20 25 30

Ala Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu His Asp Glu Pro
35 40 45

Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp Ile
50 55 60

Ser Arg His Gln Tyr His Ala Leu Pro Ala Thr Val Trp Ser Leu Gly
65 70 75 80

Ile Xaa Leu Tyr Asp Met
85

<210> 38
<211> 584
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1)..(584)
<223> n = g, a, c or t

<400> 38
aaataatcca ggcaggagaa gagaggaggg cacacttgg aactccctcc ccacaatacg 60
tgattattta catttttagta attggacaat cccggctcag gaggagggtt caagaatctg 120
caaaaatggg agggagcggc ccaggagaac aaacagcaag ctttatttcc cctagccat 180
cccccaaaaa accatccatc ccatcctagt gtctgggt gtccgggtgt gtccatcttc 240
cattccttcc caaatttatgg aagtaagggtt cttctcacca gaataagagc acttgggata 300
acagagttagg gtcccccac ccaaaaaaaaaaaaaaaa aaaaaaaaaan gaagccttgg ggtaacaaca 360
gggcattacc tccccccagaa taaaagaatcc tgggctgagg caggttaagca gcttgaccca 420
atatgggacc ctaggctagg ggaaagggtc ccttactaa aataaaaagct actggggat 480
tggaaaggaaa gcacccttgc ccaagtaaga gcatatgaac taagtttngn tgngngtagt 540
aggaggnngcc aatgtggggt gacacatcat cagaataaga gtcc 584

<210> 39
<211> 2052
<212> DNA
<213> Homo sapiens

<400> 39
cgcgcgcgc gaatctcaac gctgcgcgt ctgcggcgc ttccgggcca ccagtttctc 60
tgcttccac cctggcgcgc cccagccctg gtcctccagc tgcgtgcgc cgggcgtcca 120
cgccctgcgg gcttagcggg ttcagtggc tcaatctcgt cagcgccacc tccatgttga 180
ccaaggctct acagggggcct cccgcgcgcc cgggacccc cacgcgcgcg ccaggaggca 240
aggatcggga agcgttcgag gccgagtatc gactcgccccc cctcctgggt aaggggggct 300
ttggcaccgt ttgcgcagga caccgcctca cagatcact ccaggtggcc atcaaagtga 360
ttcccccggaa tcgtgtgcgt ggctggtccc cttgtcaga ctcagtaca tgcccactcg 420
aagtgcact gctatggaaa gtgggtgcag gtgggtggca ccctggcgtg atccgcctgc 480
ttgactgggt tgagacacag gagggttca tgctggtctt cgagcggccct ttgcccgc 540
aggatctctt tgactatatac acagagaagg gcccactggg tgaaggccca agccgctgt 600
tctttggcca agtagtggca gccatccagc actgcccattc ccgtggaggt gtccatcgtg 660
acatcaagga tgagaacatc ctgatagacc tacgcgtgg ctgtgcacaa ctcattgatt 720
tttgtctgg tgccctgctt catgatgaac cttacactga cttgtatggg acaagggtgt 780
acagccccc agagtggatc tctgacacacc agtaccatgc actcccgcc actgtctgg 840
caactggcat cctcctctat gacatgggt gtggggacat tccctttgag agggaccagg 900
agattctgga agctgagctc cactcccag cccatgtctc cccagactgc tgcgcctaa 960
tccgcggcgt cctggccccc aaaccttctt cccgaccctc actggaaagag atcctgctgg 1020
acccctggat gcaaacacca gccgaggatg taccctcaa cccctccaaa ggaggccctg 1080
ccccttggc ctggctctt ctaccctaa cctggcctgg cctggcctgg ccccaatgg 1140
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tacaggtcat taccagtcat taaagtccag tattactaag gtaagggtt gaggatcagg 1260
ggtagaaga cataaaccaa gtctgcccag ttccctccc aatcctacaa aggaccttc 1320
ctcccagaac ctgtggtccc tgattctgga ggggaactt ctgcctctc attttctaa 1380
ggaagtttat ttgggtgaag ttgtccccat tctgacccccc ggactctta ttctgatgt 1440
gtgtcaccaccc acattggcac ctcctactac caccacacaa acttagttca tatgcttta 1500

cttgggcaag	ggtgcttcc	ttccaatacc	ccagtagctt	ttatTTTgt	aaaggGaccC	1560
tttcccctag	cctagggtcc	catattgggt	caagctgctt	acctgcctca	gcccaggatt	1620
ctttattctg	ggggaggtaa	tgcCTgttG	ttacCCcaag	gcttctttt	ttttttttt	1680
tgggtgaggg	gaccctactc	tgttatccca	agtgctctta	ttctggtag	aagaacctta	1740
cttcataat	ttgggaagga	atggaagatg	gacaccacCG	gacaccacca	gacacttagga	1800
tggatggat	ggTTTTTGG	gggatgggtc	aggggaaata	aggcttgctg	tttGTTCTCC	1860
tgggcgcctc	cctccaactt	ttgcagattc	ttgcaacctc	ctcctgagcc	gggattgtcc	1920
aattactaaa	atgtaaataa	tcacgtattg	tggggaggGG	agttccaagt	gtgcctcct	1980
ctcttctcct	gcctggatta	tttaaaaAGC	catgtgtgga	aaccactat	ttaataaaag	2040
taatagaatc	ag					2052

<210> 40

<211> 311

<212> PRT

<213> Homo sapiens

<400> 40

Met	Leu	Thr	Lys	Pro	Leu	Gln	Gly	Pro	Pro	Ala	Pro	Pro	Gly	Thr	Pro
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Thr	Pro	Pro	Pro	Gly	Gly	Lys	Asp	Arg	Glu	Ala	Phe	Glu	Ala	Glu	Tyr
						20			25				30		

Arg	Leu	Gly	Pro	Leu	Leu	Gly	Lys	Gly	Gly	Phe	Gly	Thr	Val	Phe	Ala
							35		40				45		

Gly	His	Arg	Leu	Thr	Asp	Arg	Leu	Gln	Val	Ala	Ile	Lys	Val	Ile	Pro
							50		55				60		

Arg	Asn	Arg	Val	Leu	Gly	Trp	Ser	Pro	Leu	Ser	Asp	Ser	Val	Thr	Cys
						65		70			75			80	

Pro	Leu	Glu	Val	Ala	Leu	Leu	Trp	Lys	Val	Gly	Ala	Gly	Gly	His
							85		90				95	

Pro	Gly	Val	Ile	Arg	Leu	Leu	Asp	Trp	Phe	Glu	Thr	Gln	Glu	Gly	Phe
							100		105				110		

Met	Leu	Val	Leu	Glu	Arg	Pro	Leu	Pro	Ala	Gln	Asp	Leu	Phe	Asp	Tyr
							115		120				125		

Ile	Thr	Glu	Lys	Gly	Pro	Leu	Gly	Glu	Gly	Pro	Ser	Arg	Cys	Phe	Phe
							130		135				140		

Gly	Gln	Val	Val	Ala	Ala	Ile	Gln	His	Cys	His	Ser	Arg	Gly	Val	Val
							145		150				155		160

His	Arg	Asp	Ile	Lys	Asp	Glu	Asn	Ile	Leu	Ile	Asp	Leu	Arg	Arg	Gly
							165		170				175		

Cys	Ala	Lys	Leu	Ile	Asp	Phe	Gly	Ser	Gly	Ala	Leu	Leu	His	Asp	Glu
							180		185				190		

Pro	Tyr	Thr	Asp	Phe	Asp	Gly	Thr	Arg	Val	Tyr	Ser	Pro	Pro	Glu	Trp
							195		200				205		

Ile	Ser	Arg	His	Gln	Tyr	His	Ala	Leu	Pro	Ala	Thr	Val	Trp	Ser	Leu
							210		215				220		

Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile Pro Phe Glu Arg
225 230 235 240

Asp Gln Glu Ile Leu Glu Ala Glu Leu His Phe Pro Ala His Val Ser
245 250 255

Pro Asp Cys Cys Ala Leu Ile Arg Arg Cys Leu Ala Pro Lys Pro Ser
260 265 270

Ser Arg Pro Ser Leu Glu Glu Ile Leu Leu Asp Pro Trp Met Gln Thr
275 280 285

Pro Ala Glu Asp Val Pro Leu Asn Pro Ser Lys Gly Gly Pro Ala Pro
290 295 300

Leu Ala Trp Ser Leu Leu Pro
305 310

<210> 41

<211> 105

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1)..(105)

<223> n = g, a, c or t

<400> 41

ctggaactgc acntagtcggc agctctccgc ggccgcggtc tccctgggn tggtgccgta 60
cttttggatg gttttctcta cnacntcccg caagcttccn tccag 105

<210> 42

<211> 1125

<212> DNA

<213> Homo sapiens

<400> 42

gtctccccca ctgtcagcac ctcttctgtg tggtgagtgg accgcttacc ccactagg 60
aaagatgtcag cccaggagag ctgcctcagc ctcataaagt acttcttctt cgtttcaac 120
ctcttcttct tcgtcctcgg cagcctgatc ttctgcttcg gcatctggat cctcatcgac 180
aagaccagct tcgtgtcctt tgtgggcttg gccttcgtgc ctctgcagat ctggtccaa 240
gtcctggcca ttcaggaat cttcaccatg ggcattcccc tccctgggtt tggtggggcc 300
ctcaaggagc tccgctgcct cctgggcctg tattttggta tgctgctgc cctgtttgcc 360
acacagatca ccctggaaat cctcatctcc actcagcggg cccagctgga gcgaagctt 420
cgggacgtcg tagagaaaac catccaaaag tacggcacca accccgagga gaccgcggcc 480
gaggagagct gggactatgt gcagttccag ctgcgtcgat gcccgtggca ctacccgcag 540
gactggttcc aagtctcat cctgagaggt aacgggtcgg aggccgcaccc cgtgccctgc 600
tcctgctaca acttgtcggc gaccaacgc tccacaatcc tagataaggt gatcttgccc 660
cagctcagca ggcttggaca cctggcgcgg tccagacaca gtgcagacat ctgcgtgtc 720
cctgcagaga gccacatcta ccgcggggc tgcgcgcagg gcctccagaa gtggctgcac 780
aacaacctta tttccatagt gggcatttgc ctgggcgtcg gcctactcga gctcgggttc 840
atgacgctct cgtatattct gtgcagaaac ctggaccacg ttcataaccc gctcgctcg 900
taccgttagg ccccgccctc cccaaagtcc cggccccc ccgtcacgtg cgctgggcac 960
ttccctgctg cctgtaaata tttgttaat ccccgatccg cctggagccc tccgcctca 1020
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<210> 43
<211> 281
<212> PRT
<213> Homo sapiens

<400> 43
Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe
1 5 10 15

Val Phe Asn Leu Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe
20 25 30

Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly
35 40 45

Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser
50 55 60

Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
65 70 75 80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
85 90 95

Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
100 105 110

Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln
115 120 125

Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp
130 135 140

Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp
145 150 155 160

Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg
165 170 175

Val Pro Cys Ser Cys Tyr Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile
180 185 190

Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly His Leu Ala
195 200 205

Arg Ser Arg His Ser Ala Asp Ile Cys Ala Val Pro Ala Glu Ser His
210 215 220

Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn
225 230 235 240

Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
245 250 255

Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
260 265 270

Val Tyr Asn Arg Leu Ala Arg Tyr Arg
275 280

<210> 44
<211> 2915
<212> DNA
<213> Homo sapiens

<400> 44

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gccctactg cgctgctgct gctgctgctg ggccatggcg gcccggggcg ctggggcgcc 120
cgggcccgagg aggccggccgc ggcggccggcg gacggggccc cccggcaga cggcgaggac 180
ggacaggacc cgcacagcaa gcacactgtac acggccgaca tttcacgca cggatccag 240
agcggccgcgc acttcgtcat gtttgcgcg ccctgggtg gacactgcca gcggctgcag 300
ccgacttggaa atgacctggg agacaaatac aacagcatgg aagatgccaa agtctatgt 360
gctaaagtgg actgcacggc ccactccgac gtgtgcctcg cccaggggt gcgaggatac 420
cccacctaagctttcaa gccaggccaa gaagctgtga agtaccaggg tcctcggac 480
ttccagacac tggaaaactg gatgctgcag acactgaacg aggagccagt gacaccagag 540
ccggaagtgg aaccgccccag tgcccccgag ctcagaacg ggctgtatga gctctcagca 600
agcaactttg agctgcacgt tgcaacaaggc gaccaccca tcaagttctt cgctccgtgg 660
tgtggtaact gcaaaggccct ggctccaacc tgggagcagc tggctctggg cttgaacat 720
tccgaaaactg tcaagattgg caaggttgat tgtacacagc actatgaact ctgctccgga 780
aaccaggttc gtggctatcc cactttctc tggttccgag atggggaaaaaa ggtggatcag 840
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gccgaagttag actgcactgc tgaacggaat atctgcagca agtattcggt acgaggctac 1200
cccacgttat tgctttcgcg aggagggaaag aaagtcaactg agcacagctgg aggccagagac 1260
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agctttgcacat cacgacttgc ttttccaaat gggataactt ttttctgtt 2880
caactatgtatc ttttctgtt aactccctt tttt 2915

<210> 45
<211> 432
<212> PRT
<213> Homo sapiens

<400> 45
 Met Pro Ala Arg Pro Gly Arg Leu Leu Pro Leu Leu Ala Arg Pro Ala
 1 5 10 15
 Ala Leu Thr Ala Leu Leu Leu Leu Leu Gly His Gly Gly Gly
 20 25 30
 Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Asp Gly
 35 40 45
 Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro His Ser Lys His
 50 55 60
 Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile Gln Ser Ala Ala His
 65 70 75 80
 Phe Val Met Phe Phe Ala Pro Trp Cys Gly His Cys Gln Arg Leu Gln
 85 90 95
 Pro Thr Trp Asn Asp Leu Gly Asp Lys Tyr Asn Ser Met Glu Asp Ala
 100 105 110
 Lys Val Tyr Val Ala Lys Val Asp Cys Thr Ala His Ser Asp Val Cys
 115 120 125
 Ser Ala Gln Gly Val Arg Gly Tyr Pro Thr Leu Lys Leu Phe Lys Pro
 130 135 140
 Gly Gln Glu Ala Val Lys Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu
 145 150 155 160
 Glu Asn Trp Met Leu Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu
 165 170 175
 Pro Glu Val Glu Pro Pro Ser Ala Pro Glu Leu Lys Gln Gly Leu Tyr
 180 185 190
 Glu Leu Ser Ala Ser Asn Phe Glu Leu His Val Ala Gln Gly Asp His
 195 200 205
 Phe Ile Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala
 210 215 220
 Pro Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val
 225 230 235 240
 Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser Gly
 245 250 255
 Asn Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp Gly Lys
 260 265 270
 Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser Leu Arg Glu
 275 280 285
 Tyr Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly Ala Thr Glu Thr
 290 295 300
 Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala Glu Pro Glu Ala Asp
 305 310 315 320

Lys Gly Thr Val Leu Ala Leu Thr Glu Asn Asn Phe Asp Asp Thr Ile
325 330 335

Ala Glu Gly Ile Thr Phe Ile Lys Phe Tyr Ala Pro Trp Cys Gly His
340 345 350

Cys Arg Thr Leu Ala Pro Thr Trp Glu Glu Leu Ser Lys Lys Glu Phe
355 360 365

Pro Gly Leu Ala Gly Val Lys Ile Ala Glu Val Asp Cys Thr Ala Glu
370 375 380

Arg Asn Ile Cys Ser Lys Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu
385 390 395 400

Leu Phe Arg Gly Gly Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp
405 410 415

Leu Asp Ser Leu His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu
420 425 430

<210> 46

<211> 551

<212> DNA

<213> Homo sapiens

<400> 46

ccagccatgt acagaaaaaa gagtgaatgt gccttaaga agaagagcaa tgagacacag 60
tgttcaact tcatccgtgt cctggttct tacaatgtca cccatctcta cacctgcggc 120
accttcgcct tcagccctgc ttgtaccttc attgaacttc aagattccta cctgtgccc 180
atctcgagg acaaggtcat ggagggaaaa ggccaaagcc ccttgaccgc cgctcacaag 240
catacggctg tcttggtggaa tggatgctc tattctggta ctatgaacaa cttccctggc 300
agtgagccca tcctgtatgcg cacactggaa tcccagctg tcctcaagac cgacaacttc 360
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tacttcttct tcgaggagac agccagcggag tttgacttct ttgagaggct ccacacatcg 480
cgggtggcta gagtctgcaa gaatgacgtg ggccggcgaaa agctgctgca gaagaagtgg 540
accacccatcc t 551

<210> 47

<211> 3252

<212> DNA

<213> Homo sapiens

<400> 47

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atgccccacc cctgccacca atacacacgc ttctgtgcc tggggctctc ctattggtcc 120
tcggggggat gtggtaagaa ctgctcaccc agaaagtgcc cgggtgcctg tttcccccaga 180
cctcccttgt gacagtctgt ggctgagcat ggcctccca gccctggcc tggaccctcg 240
gagccctcctg ggcctttcc tcttccaact gcttcagctg ctgctgccga cgacgaccgc 300
ggggggagggc gggcaggggc ccatgcccag ggtcagatac tatgcaggggg atgaacgtag 360
ggcactttagc ttcttccacc agaaggccct ccaggatttt gacactctgc tcctgagtgg 420
tcatggaaat actctctacg tgggggctcg agaaggcatt ctggccttgg atatccagga 480
tccaggggtc cccaggctaa agaacatgt accgtggcca gccagtgaca gaaaaaaagag 540
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 ggacaccaac actcccttcccccagggtca tgcaggatc tgctccctcc tgcttccctt 3000
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 agccttcttcc actcccttac cctagctgttgc cccttcaccccttcccttcc cttttcttctt 3180
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 cttatgtatc at 3252

<210> 48

<211> 762

<212> PRT

<213> Homo sapiens

<400> 48

Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly Leu
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Phe Leu Phe Gln Leu Leu Gln Leu Leu Pro Thr Thr Thr Ala Gly
 20 25 30

Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr Ala Gly Asp
 35 40 45

Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly Leu Gln Asp Phe
 50 55 60

Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr Leu Tyr Val Gly Ala
 65 70 75 80

Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln Asp Pro Gly Val Pro Arg
 85 90 95

Leu Lys Asn Met Ile Pro Trp Pro Ala Ser Asp Arg Lys Lys Ser Glu
 100 105 110

Cys Ala Phe Lys Lys Ser Asn Glu Thr Gln Cys Phe Asn Phe Ile
 115 120 125

Arg Val Leu Val Ser Tyr Asn Val Thr His Leu Tyr Thr Cys Gly Thr
 130 135 140

Phe Ala Phe Ser Pro Ala Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr
 145 150 155 160

Leu Leu Pro Ile Ser Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser
 165 170 175

Pro Phe Asp Pro Ala His His Thr Ala Val Leu Val Asp Gly Met
 180 185 190

Leu Tyr Ser Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu
 195 200 205

Met Arg Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu
 210 215 220

Arg Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
 225 230 235 240

Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp Phe
 245 250 255

Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys Asn Asp
 260 265 270

Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr Phe Leu Lys
 275 280 285

Ala Gln Leu Leu Ser Ala Pro Ser Arg Gly Ser Cys Pro Ser Thr Ser
 290 295 300

Ser Ala Thr Arg Ser Cys Ser Pro Pro Ile Leu Pro Gln Leu Pro Thr
 305 310 315 320

Ser Thr Gln Ser Ser Pro Pro Ser Gly Gln Val Gly Gly Thr Arg Ser
 325 330 335

Ser Ala Val Cys Ala Phe Ser Leu Leu Asp Ile Glu Arg Val Phe Lys
 340 345 350

Gly Lys Phe Lys Glu Leu Asn Lys Glu Thr Ser Arg Trp Thr Thr Tyr
 355 360 365

Arg Gly Pro Glu Thr Asn Pro Arg Pro Gly Ser Cys Ser Val Gly Pro
 370 375 380

Ser Ser Asp Lys Ala Leu Thr Phe Met Lys Asp His Phe Leu Met Asp
 385 390 395 400
 Glu Gln Val Val Gly Thr Pro Leu Leu Val Lys Ser Gly Val Glu Tyr
 405 410 415
 Thr Arg Leu Ala Val Glu Thr Ala Gln Gly Leu Asp Gly His Ser His
 420 425 430
 Leu Val Met Tyr Leu Gly Thr Thr Gly Ser Leu His Lys Ala Val
 435 440 445
 Val Ser Gly Asp Ser Ser Ala His Leu Val Glu Glu Ile Gln Leu Phe
 450 455 460
 Pro Asp Pro Glu Pro Val Arg Asn Leu Gln Leu Ala Pro Thr Gln Gly
 465 470 475 480
 Ala Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala
 485 490 495
 Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg Asp
 500 505 510
 Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu Leu Ser
 515 520 525
 Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg Gly Asn Pro
 530 535 540
 Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser Leu Arg Pro Gln
 545 550 555 560
 Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala Val Pro Asn Ser Ile
 565 570 575
 Leu Glu Leu Pro Cys Pro His Leu Ser Ala Leu Ala Ser Tyr Tyr Trp
 580 585 590
 Ser His Gly Pro Ala Ala Val Pro Glu Ala Ser Ser Thr Val Tyr Asn
 595 600 605
 Gly Ser Leu Leu Leu Ile Val Gln Asp Gly Val Gly Gly Leu Tyr Gln
 610 615 620
 Cys Trp Ala Thr Glu Asn Gly Phe Ser Tyr Pro Val Ile Ser Tyr Trp
 625 630 635 640
 Val Asp Ser Gln Asp Gln Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly
 645 650 655
 Ile Pro Arg Glu His Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly
 660 665 670
 Ala Ala Leu Ala Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val
 675 680 685
 Thr Val Leu Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val
 690 695 700

Ala Ser Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys
705 710 715 720

Glu Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp Ala
740 745 750

Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 49

<211> 182

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1)..(182)

<223> n = g, a, c or t

<400> 49

accagcagtc ctgcggcacc tacctccgct tgcgccagcc gcccccagg cccttcctgg 60
acatggggga gggcaccaag aaccgaatca tcacagccga ggggatcatc ctcctgttct 120
gcgcgggtggc gcctgggacg ctgctgctgt tnagggaaacg atggcaagaa cganaactcn 180
gg 182

<210> 50

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (1)..(60)

<223> Xaa = any amino acid

<400> 50

Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro Pro Pro Arg
1 5 10 15

Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala
20 25 30

Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu
35 40 45

Leu Xaa Arg Lys Arg Trp Gln Glu Arg Xaa Leu Xaa
50 55 60

<210> 51

<211> 182

<212> DNA

<213> Homo sapiens

<220>
<221> modified_base
<222> (1)..(182)
<223> n = g, a, c or t

<400> 51
accagcagtc ctgcggcacc tacctcccg tgcgccagcc gcccccagg cccttcctgg 60
acatggggga gggcaccaag aaccgaatca tcacagccga ggggatcatc ctccctgttct 120
gcgcgggtggt gcctgggacg ctgctgctgt tnagggaaacg atggcaagaa cganaactcn 180
gg 182

<210> 52
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (1)..(60)
<223> Xaa = any amino acid

<400> 52
Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro Pro Pro Arg
1 5 10 15

Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala
20 25 30

Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu
35 40 45

Leu Xaa Arg Lys Arg Trp Gln Glu Arg Xaa Leu Xaa
50 55 60

<210> 53
<211> 1107
<212> DNA
<213> Homo sapiens

<400> 53
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caagctctgc ctgccaccaat cttccctcctc ttccctgtgt ctgctgtcta cctggccct 120
gggtgccagg ccctgtggat gcacaaggc ccagcatcat tgatggtagg cctggggaa 180
gacgcccact tccaatgcc gcacaatagc agcaacaacg ccaacgtcac ctgggtggc 240
gtcctccatg gcaactacac gtggccccct gagttcttgg gcccggcga ggaccccaat 300
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caggagggca acgagtcatc ccagcagtcc tgccgcaccc acctccgcgt ggcgcagcc 420
ccccccaggc cttccctgga catgggggag ggcaccaaga accgaatcat cacagccgag 480
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tggcagaacg agaagctcg gttggatgcc ggggatgaat atgaagatga aaacctttat 600
gaaggcctga acctggacga ctgctccatg tatgaggaca tctcccgggg cctccaggc 660
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tgccttccc aggctccctt caccagccg gtaatgagcc ctaaatcgct gcctctaggg 1020
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tagtataat aaattcttcc caactgc 1107

<210> 54
<211> 226
<212> PRT
<213> Homo sapiens

<400> 54
Met Pro Gly Gly Pro Gly Val Leu Gln Ala Leu Pro Ala Thr Ile Phe
1 5 10 15

Leu Leu Phe Leu Leu Ser Ala Val Tyr Leu Gly Pro Gly Cys Gln Ala
20 25 30

Leu Trp Met His Lys Val Pro Ala Ser Leu Met Val Ser Leu Gly Glu
35 40 45

Asp Ala His Phe Gln Cys Pro His Asn Ser Ser Asn Asn Ala Asn Val
50 55 60

Thr Trp Trp Arg Val Leu His Gly Asn Tyr Thr Trp Pro Pro Glu Phe
65 70 75 80

Leu Gly Pro Gly Glu Asp Pro Asn Gly Thr Leu Ile Ile Gln Asn Val
85 90 95

Asn Lys Ser His Gly Gly Ile Tyr Val Cys Arg Val Gln Glu Gly Asn
100 105 110

Glu Ser Tyr Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro
115 120 125

Pro Pro Arg Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile
130 135 140

Ile Thr Ala Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly
145 150 155 160

Thr Leu Leu Leu Phe Arg Lys Arg Trp Gln Asn Glu Lys Leu Gly Leu
165 170 175

Asp Ala Gly Asp Glu Tyr Glu Asp Glu Asn Leu Tyr Glu Gly Leu Asn
180 185 190

Leu Asp Asp Cys Ser Met Tyr Glu Asp Ile Ser Arg Gly Leu Gln Gly
195 200 205

Thr Tyr Gln Asp Val Gly Ser Leu Asn Ile Gly Asp Val Gln Leu Glu
210 215 220

Lys Pro
225

<210> 55
<211> 1038
<212> DNA
<213> Homo sapiens

<400> 55
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ccatggggca tcattctgga gtcctggcc atactggca tcgtggtcac aattctgcta 120
ctcttagcat ttcttcttcatgcgaaag atccaagact gcagccagtg gaatgtcctc 180

cccacccagc tccttcttctt cctgagtgtc ctggggctct tcggactcgc ttttgccttc 240
 atcatcgagc tcaatcaaca aactgcccccc gtacgctact ttctctttgg gtttctcttt 300
 gctctctgtt ttcattgcct cttagctcat gcctccaatc tagtgaagct gtttcggggt 360
 tgtgtctcct ttccttgac gacaattctg tgcatgtca ttggttgcag tctgttcaa 420
 atcattattt ccactgagta tttgtacttc atcatgacca gaggtatgat gtttgcata 480
 atgacaccct gccagctcaa tttgtacttt gttgtactcc tttgttatgt cttcttcctg 540
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 cagcatggaa ggctcatctt tttactgtg ctcttcctca tttatcatctg gttgggtgtgg 660
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 gtcgtctgca ttgtcttggt caccaacgcgca tgggtttcc tttgtctgtatcatcgccct 780
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 gacagtgtatg gagctgagga ggatgttagca tttacttcat atggtaactcc catteagccg 960
 cagactgttg atccccacaca agagtgtttc atccccacagg cttaaaactaag ccccccagcaa 1020
 gatgcaggag gatgtataa 1038

<210> 56

<211> 345

<212> PRT

<213> Homo sapiens

<400> 56

Met Tyr Lys Asp Cys Ile Glu Ser Thr Gly Asp Tyr Phe Leu Leu Cys
 1 5 10 15

Asp Ala Glu Gly Pro Trp Gly Ile Ile Leu Glu Ser Leu Ala Ile Leu
 20 25 30

Gly Ile Val Val Thr Ile Leu Leu Leu Ala Phe Leu Phe Leu Met
 35 40 45

Arg Lys Ile Gln Asp Cys Ser Gln Trp Asn Val Leu Pro Thr Gln Leu
 50 55 60

Leu Phe Leu Leu Ser Val Leu Gly Leu Phe Gly Leu Ala Phe Ala Phe
 65 70 75 80

Ile Ile Glu Leu Asn Gln Gln Thr Ala Pro Val Arg Tyr Phe Leu Phe
 85 90 95

Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu Leu Ala His Ala Ser
 100 105 110

Asn Leu Val Lys Leu Val Arg Gly Cys Val Ser Phe Ser Trp Thr Thr
 115 120 125

Ile Leu Cys Ile Ala Ile Gly Cys Ser Leu Leu Gln Ile Ile Ile Ala
 130 135 140

Thr Glu Tyr Val Thr Leu Ile Met Thr Arg Gly Met Met Phe Val Asn
 145 150 155 160

Met Thr Pro Cys Gln Leu Asn Val Asp Phe Val Val Leu Leu Val Tyr
 165 170 175

Val Leu Phe Leu Met Ala Leu Thr Phe Phe Val Ser Lys Ala Thr Phe
 180 185 190

Cys Gly Pro Cys Glu Asn Trp Lys Gln His Gly Arg Leu Ile Phe Ile
 195 200 205

Thr Val Leu Phe Ser Ile Ile Trp Val Val Trp Ile Ser Met Leu
 210 215 220
 Leu Arg Gly Asn Pro Gln Phe Gln Arg Gln Pro Gln Trp Asp Asp Pro
 225 230 235 240
 Val Val Cys Ile Ala Leu Val Thr Asn Ala Trp Val Phe Leu Leu Leu
 245 250 255
 Tyr Ile Val Pro Glu Leu Cys Ile Leu Tyr Arg Ser Cys Arg Gln Glu
 260 265 270
 Cys Pro Leu Gln Gly Asn Ala Cys Pro Val Thr Ala Tyr Gln His Ser
 275 280 285
 Phe Gln Val Glu Asn Gln Glu Leu Ser Arg Ala Arg Asp Ser Asp Gly
 290 295 300
 Ala Glu Glu Asp Val Ala Leu Thr Ser Tyr Gly Thr Pro Ile Gln Pro
 305 310 315 320
 Gln Thr Val Asp Pro Thr Gln Glu Cys Phe Ile Pro Gln Ala Lys Leu
 325 330 335
 Ser Pro Gln Gln Asp Ala Gly Gly Val
 340 345

<210> 57
 <211> 2457
 <212> DNA
 <213> Homo sapiens

<400> 57
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 cgaatcccgag ccgagcggag aggaatccgg cagtagagag cggactccag ccggcggacc 120
 ctgcagccct cgcctgggac agccgcgcgc tggcggcggc cccaagagag catcgagcag 180
 cggAACCCGc gaagccggcc cgcagccgcg accccgcgcag cctgcccgtc tcccgcggcc 240
 ggtccgggca gcatgaggcg cgccggcgctc tggctctggc tggcgcgcgt ggcgctgagc 300
 ctgcagccgg ccctggccca aatttgtggct actaatttgc cccctgaaga tcaagatggc 360
 tctgggatg actctgacaa ctttcggc tcaggtgcag gtgcgttgc agatatcacc 420
 ttgtcacagc agacccccctc cacttggaaag gacacgcgc tccgtacggc tattccacg 480
 tctccagaac ccaccggcct ggaggctaca gtcgcctcca cctccaccct gccggctgga 540
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 cgggagcagg aggccacccc ccgacccagg gagaccacac agctccgcac cactcatcag 660
 gccttaacga ccacagccac cacggcccaag gagccgcac cctccaccct ccacaggac 720
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 actccccaca cagaggatgg aggtccttgc gccacccaga ggctgtctga ggatggagcc 840
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 cagggggccca cgggggcctc acagggcctc ctggacagga aagaggtgt gggaggggtc 1020
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 cgcataaga agaaggacga aggcagctac tccttgagg acccgaaaaca agccaaacggc 1140
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 cctggccctcc cctgccaacca ggcacccctcc ccagcattcc agccctctg gtcgctcctg 1320
 cccacggagt cgtgggggtgt gctgggagct ccactctgtc tctctgactt ctgcctggag 1380
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 ggggagggggg atccgactgc tttggaccta aatggcctca tggcgtggag agatcctgcg 1560
 ggtggggctt gggcataca cacctgttagc acttactggt aggaccaagc atcttggggg 1620

gggtggccgct	gagtggcagg	ggacaggagt	ccactttgtt	tcgtggggag	gtctaattcta	1680
gatatcgact	tgtttttgca	catgtttcct	ctagttctt	gttcatagcc	cagtagacct	1740
tgttacttct	gaggtaagtt	aagtaagttg	atccggtata	ccccccatctt	gcttcctaa	1800
tctatggtcg	ggagacagca	tcagggtaa	gaagactttt	ttttttttt	tttttaaact	1860
aggagaacca	aatcttggaa	ccaaaatgtt	ggcttagttt	gtgtgttgc	tcttgagtt	1920
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tgttggcagg	ctggccagtc	caggctgccg	tggggccgcc	gcctcttca	agcagtcgtg	2040
cctgtgtcca	tgcgctcagg	gccatgtga	ggcctgggcc	gctgccacgt	tggagaagcc	2100
cgtgtgagaa	gtgaatgtc	ggactcagcc	tccagacaga	gaggactgtt	gggagggcgg	2160
caggggcctg	gagatcctcc	tgcagaccac	gccccgtctg	cctgtggcgc	cgtctccagg	2220
ggctgtttcc	tcctggaaat	tgacgagggg	tgtcttggc	agagctggct	ctgagcgcct	2280
ccatccaaagg	ccaggttctc	cgttagctcc	tgtggcccca	ccctgggccc	tgggctggaa	2340
tcaggaatat	tttccaaaga	gtgatagtct	tttgctttt	gcaaaaactct	acttaatcca	2400
atgggtttt	ccctgtacag	tagatttcc	aaatgtata	aactttaata	taaagta	2457

<210> 58

<211>.310

<212> PRT

<213> Homo sapiens

<400> 58

Met Arg Arg Ala Ala Leu Trp Leu Trp Leu Cys Ala Leu Ala Leu Ser
 1 5 10 15

Leu Gln Pro Ala Leu Pro Gln Ile Val Ala Thr Asn Leu Pro Pro Glu
20 25 30

Asp Gln Asp Gly Ser Gly Asp Asp Ser Asp Asn Phe Ser Gly Ser Gly
35 40 45

Ala Gly Ala Leu Gln Asp Ile Thr Leu Ser Gln Gln Thr Pro Ser Thr
 50 55 60

Trp Lys Asp Thr Gln Leu Leu Thr Ala Ile Pro Thr Ser Pro Glu Pro
65 70 75 80

Thr Gly Leu Glu Ala Thr Ala Ala Ser Thr Ser Thr Leu Pro Ala Gly
85 90 95

Glu Gly Pro Lys Glu Gly Glu Ala Val Val Leu Pro Glu Val Glu Pro
 100 105 110

Gly Leu Thr Ala Arg Glu Gln Glu Ala Thr Pro Arg Pro Arg Glu Thr
115 120 125

Thr Gln Leu Pro Thr Thr His Gln Ala Ser Thr Thr Thr Ala Thr Thr
 130 135 140

Ala Gln Glu Pro Ala Thr Ser His Pro His Arg Asp Met Gln Pro Gly
145 150 155 160

His His Glu Thr Ser Thr Pro Ala Gly Pro Ser Gln Ala Asp Leu His
165 170 175

Thr Pro His Thr Glu Asp Gly Gly Pro Ser Ala Thr Glu Arg Ala Ala
 180 185 190

Glu Asp Gly Ala Ser Ser Gln Leu Pro Ala Ala Glu Gly Ser Gly Glu
195 200 205

Gln Asp Phe Thr Phe Glu Thr Ser Gly Glu Asn Thr Ala Val Val Ala
210 215 220

Val Glu Pro Asp Arg Arg Asn Gln Ser Pro Val Asp Gln Gly Ala Thr
225 230 235 240

Gly Ala Ser Gln Gly Leu Leu Asp Arg Lys Glu Val Leu Gly Gly Val
245 250 255

Ile Ala Val Gly Leu Val Gly Leu Ile Phe Ala Val Cys Leu Val Gly
260 265 270

Phe Met Leu Tyr Arg Met Lys Lys Asp Glu Gly Ser Tyr Ser Leu
275 280 285

Glu Glu Pro Lys Gln Ala Asn Gly Gly Ala Tyr Gln Lys Pro Thr Lys
290 295 300

Gln Glu Glu Phe Tyr Ala
305 310

<210> 59

<211> 357

<212> DNA

<213> Homo sapiens

<400> 59

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tctgtttca cccggagcga gctcaagttc tccccacagt ggagtcacca tgggaagatt 300
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<210> 60

<211> 3260

<212> DNA

<213> Homo sapiens

<400> 60

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<210> 61
 <211> 847
 <212> PRT
 <213> Homo sapiens

<400> 61
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Ala Phe Ser Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu
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Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala
 35 40 45

Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr
 50 55 60

Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr
 65 70 75 80

Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly
 85 90 95

Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn
 100 105 110

 Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp
 115 120 125

 Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His
 130 135 140

 Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr
 145 150 155 160

 Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp
 165 170 175

 Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser
 180 185 190

 Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro
 195 200 205

 Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala
 210 215 220

 Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His
 225 230 235 240

 Thr Pro Lys Leu Glu Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg
 245 250 255

 Glu Gly Asp Ser Val Thr Met Thr Cys Glu Val Ser Ser Asn Pro
 260 265 270

 Glu Tyr Thr Thr Val Ser Trp Leu Lys Asp Gly Thr Ser Leu Lys Lys
 275 280 285

 Gln Asn Thr Phe Thr Leu Asn Leu Arg Glu Val Thr Lys Asp Gln Ser
 290 295 300

 Gly Lys Tyr Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser
 305 310 315 320

 Glu Glu Val Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val
 325 330 335

 Gln Ile Leu His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu
 340 345 350

 Cys Met Ser Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His
 355 360 365

 Asn Gly Lys Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro
 370 375 380

 Lys Ile Leu Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn
 385 390 395 400

 Ile Leu Gly Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln
 405 410 415

Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile
 420 425 430

Arg Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn
 435 440 445

Pro Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu
 450 455 460

Pro Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr
 465 470 475 480

Thr Ile Ala Cys Ala Arg Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro
 485 490 495

Val Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys
 500 505 510

Ile Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln
 515 520 525

Cys Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu
 530 535 540

Lys Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser
 545 550 555 560

Ile Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser
 565 570 575

Ile Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala
 580 585 590

Pro Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu
 595 600 605

Gly Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val
 610 615 620

Ser His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro His His
 625 630 635 640

Ser Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala
 645 650 655

Tyr Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu
 660 665 670

Ser Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val
 675 680 685

Ala Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys
 690 695 700

Gly Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly
 705 710 715 720

Leu Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys
 725 730 735

Val Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr
740 745 750

Asn Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro
755 760 765

Glu Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln
770 775 780

Arg Pro Pro Arg Thr Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His
785 790 795 800

Lys Arg Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu
805 810 815

Asp Glu Gly Ile His Tyr Ser Glu Leu Ile Gln Phe Gly Val Gly Glu
820 825 830

Arg Pro Gln Ala Gln Glu Asn Val Asp Tyr Val Ile Leu Lys His
835 840 845

<210> 62

<211> 340

<212> DNA

<213> Homo sapiens

<400> 62

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cacctacaga ccacttcact tcccctgtcc gcagcgtaac tatgtcctca tagttggctg 180
tctggtaat gtccaggccccgttaggtgt gatcttccttc catgccagcc ttgctgtcat 240
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<210> 63

<211> 79

<212> PRT

<213> Homo sapiens

<400> 63

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20 25 30

Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly
35 40 45

Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
50 55 60

Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu
65 70 75

<210> 64
<211> 340
<212> DNA
<213> Homo sapiens

<400> 64
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cacctacaga ccacttcaact tcccctgtcc gcagcgtaac tatgtcctca taggtggctg 180
tctggtaat gtccaggccc tcgttaggtgt gatcttcctc catgccagcc ttgctgtcat 240
ccttgccag cagcaggaag ataggcacga tgatgaagag gatgatcagc agcgtctgga 300
tcatgatgat accatccttc agcgtgttcc tctgcttcag 340

<210> 65
<211> 1226
<212> DNA
<213> Homo sapiens

<400> 65
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gccagatcg aggaccggta ccggaatccc aaaggttagt cttgttcgcg gatctggcag 180
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acctcggagg tctaccaggg ctgcggcaca gagctgcgag tcatgggatt cagcacctt 480
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<210> 66
<211> 229
<212> PRT
<213> Homo sapiens

<400> 66
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20 25 30

Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg Ile Trp Gln
35 40 45

Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys Met His
50 55 60

Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu Trp Lys Gln
 65 70 75 80
 Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly Arg Met
 85 90 95
 Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile Gln Gly Ile
 100 105 110
 Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys Cys Asn Asn
 115 120 125
 Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val Met Gly
 130 135 140
 Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly
 145 150 155 160
 Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val Pro
 165 170 175
 Ile Phe Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly Met Glu Glu
 180 185 190
 Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu
 195 200 205
 Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu
 210 215 220
 His Pro Gly Gln Glu
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<210> 67
 <211> 449
 <212> DNA
 <213> Homo sapiens

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<400> 67
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 tagtggagct catttacaaa taggcatgcc tcacacacac agtccaaagg caagacactg 300
 gcttggaaat taggctcatg atgtgattcc tattatatgt acctgatttt tttaggcccc 360
 aggtatgtgg accagaggtt atgtcatgac tcttcaaaga tatgatgaaa agttgcccta 420
 gaaatctaga gatgcatttt tatttaatt 449

<210> 68
 <211> 2359
 <212> DNA
 <213> Homo sapiens

<400> 68

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ttatgctaac ctctgttgc ttagtgcacatg tcctcaggac tctgatatta aaactcaatc 180
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gagtgaaatc tgaacgctgt cttatattaa gcagtagaa taggtattat cataaaaaagt 420
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ctgcagaagg ttgccttta accccagtgg ttctaaagggt tggaatttag tgaccctaat 600
atttacataa gagacttgtt ttagtggac ataaggagg ggcataagtt acaccgttt 660
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ctatgcaccc ggtaaaaaaaaaa 2359

<210> 69

<211> 240

<212> DNA

<213> Homo sapiens

<400> 69

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ggtccaaatc attatgccaa agggccgtc taggagggtt ttgttccaag tattgagatt 180
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<210> 70

<211> 980

<212> DNA

<213> Homo sapiens

<400> 70

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gactccggcc agcccgagt atgcgatcca aagagcactc cccggtagga aattgccccg 420
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gccctgcctc agtcacaccc ggaagctgac tggccacgc acagctgaag catgaggaaa 660
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cttcctcaga ctgagaactg tttccagttt atacatcaag tcactgaggt aggacaaaag 780
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<210> 71

<211> 118

<212> PRT

<213> Homo sapiens

<400> 71

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Ala Ser Leu Arg Arg Thr Pro Ala Ser Pro Ser Asp Ala Ile Gln Arg
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Ala Leu Pro Gly Arg Lys Leu Pro Arg Trp Asn Ala Ser Pro Glu Gln
35 40 45

Arg Val Ala Val Pro Cys Gly Gly Leu Thr Gln Trp Leu Asn Thr Gly
50 55 60

Lys Glu Leu Ala Leu Gly Val Arg Thr Ser Glu Thr Cys Arg Leu Gly
65 70 75 80

Ala Val His Gly Trp Glu Gln Leu His Gln Pro Leu Gln Ser Asp Ser
85 90 95

Glu Glu Asp Asp Lys Pro Cys Ser Ser His Thr Arg Lys Leu Thr Gly
100 105 110

Pro Arg Thr Ala Glu Ala
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<210> 72

<211> 531

<212> DNA

<213> Homo sapiens

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<221> modified_base

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<223> n = g, a, c or t

<400> 72

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<210> 73

<211> 1956

<212> DNA

<213> Homo sapiens

<400> 73

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<210> 74

<211> 444

<212> PRT

<213> Homo sapiens

<400> 74

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Ser Asn Cys Phe Tyr Phe Gln Ala Phe Leu Asp Glu Phe Thr Asn Trp
 20 25 30

Ser Arg Ile Asn Pro Asn Lys Ala Arg Ile Pro Met Ala Gly Asp Thr
 35 40 45

Gln Gly Val Val Gly Thr Val Ser Lys Pro Cys Phe Thr Ala Tyr Glu
 50 55 60

Met Lys Ile Gly Ala Ile Thr Phe Gln Val Ala Thr Gly Asp Ile Ala
 65 70 75 80

Thr Glu Gln Val Asp Val Ile Val Asn Ser Thr Ala Arg Thr Phe Asn
 85 90 95

Arg Lys Ser Gly Val Ser Arg Ala Ile Leu Glu Gly Ala Gly Gln Ala
 100 105 110

Val Glu Ser Glu Cys Ala Val Leu Ala Ala Gln Pro His Arg Asp Phe
 115 120 125

Ile Ile Thr Pro Gly Gly Cys Leu Lys Cys Lys Ile Ile Ile His Val
 130 135 140

Pro Gly Gly Lys Asp Val Arg Lys Thr Val Thr Ser Val Leu Glu Glu
 145 150 155 160

Cys Glu Gln Arg Lys Tyr Thr Ser Val Ser Leu Pro Ala Ile Gly Thr
 165 170 175

Gly Asn Ala Gly Lys Asn Pro Ile Thr Val Ala Asp Asn Ile Ile Asp
 180 185 190

Ala Ile Val Asp Phe Ser Ser Gln His Ser Thr Pro Ser Leu Lys Thr
 195 200 205

Val Lys Val Val Ile Phe Gln Pro Glu Leu Leu Asn Ile Phe Tyr Asp
 210 215 220

Ser Met Lys Lys Arg Asp Leu Ser Ala Ser Leu Asn Phe Gln Ser Thr
 225 230 235 240

Phe Ser Met Thr Thr Cys Asn Leu Pro Glu His Trp Thr Asp Met Asn
 245 250 255

His Gln Leu Phe Cys Met Val Gln Leu Glu Pro Gly Gln Ser Glu Tyr
 260 265 270

Asn Thr Ile Lys Asp Lys Phe Thr Arg Thr Cys Ser Ser Tyr Ala Ile
 275 280 285

Glu Lys Ile Glu Arg Ile Gln Asn Ala Phe Leu Trp Gln Ser Tyr Gln
 290 295 300

Val Lys Lys Arg Gln Met Asp Ile Lys Asn Asp His Lys Asn Asn Glu
 305 310 315 320

Arg Leu Leu Phe His Gly Thr Asp Ala Asp Ser Val Pro Tyr Val Asn
 325 330 335

Gln His Gly Phe Asn Arg Ser Cys Ala Gly Lys Asn Ala Val Ser Tyr
340 345 350

Gly Lys Gly Thr Tyr Phe Ala Val Asp Ala Ser Tyr Ser Ala Lys Asp
355 360 365

Thr Tyr Ser Lys Pro Asp Ser Asn Gly Arg Lys His Met Tyr Val Val
370 375 380

Arg Val Leu Thr Gly Val Phe Thr Lys Gly Arg Ala Gly Leu Val Thr
385 390 395 400

Pro Pro Pro Lys Asn Pro His Asn Pro Thr Asp Leu Phe Asp Ser Val
405 410 415

Thr Asn Asn Thr Arg Ser Pro Lys Leu Phe Val Val Phe Phe Asp Asn
420 425 430

Gln Ala Tyr Pro Glu Tyr Leu Ile Thr Phe Thr Ala
435 440

<210> 75

<211> 449

<212> DNA

<213> Homo sapiens

<400> 75

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<210> 76

<211> 79

<212> PRT

<213> Homo sapiens

<400> 76

Arg Ser His Leu Thr Leu Leu Tyr Cys Ser Ala Val Lys Ser Ala Ser
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Phe Thr Gly Gly Lys Gly Pro Gln Ser Leu Arg Arg Ala Ser Leu Glu
20 25 30

Thr Gly Trp Phe Phe Leu Cys Ser Pro Glu Ser Pro Ser Asp Glu Lys
35 40 45

Gly Gly Leu Glu Thr Glu Cys Gln Lys Pro Ile Lys Gly Thr Ala Leu
50 55 60

His Phe Arg Glu Gly Ala Gly Leu Glu Lys Asn Gln Arg Ser Ser
65 70 75

<210> 77
<211> 3067
<212> DNA
<213> Homo sapiens

<400> 77

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<210> 78
<211> 554
<212> DNA
<213> *Homo sapiens*

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<220>
<221> modified_base
<222> (1)..(554)
<223> n = g, a, c or t
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<210> 79
<211> 3243
<212> DNA
<213> *Homo sapiens*

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<210> 80

<211> 755

<212> PRT

<213> Homo sapiens

<400> 80

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 20 25 30

Glu Asn Phe Ser Phe Arg His Leu Glu Leu Leu Asn Leu Thr Ser Tyr
 35 40 45

Lys Cys Lys Leu Leu Ile Leu Ser Asn Ser Leu Leu Arg Asp Leu Thr
 50 55 60

Pro Lys Lys Cys Gln Phe Leu Glu Lys Ile Leu His Ser Pro Lys Ser
 65 70 75 80

Val Val Thr Leu Leu Cys Gly Val Lys Ser Ser Asp Gln Leu Tyr Glu
 85 90 95

Leu Leu Asn Ile Ser Gln Ser Arg Trp Glu Ile Ser Thr Glu Gln Glu
 100 105 110

Pro Glu Asp Tyr Ile Ser Val Ile Gln Ser Ile Ile Phe Lys Asp Ser
 115 120 125

Glu Asp Tyr Phe Glu Val Asn Ile Pro Thr Asp Leu Arg Ala Lys His
 130 135 140

Ser Gly Glu Ile Ser Glu Arg Lys Glu Ile Glu Glu Leu Ser Glu Ala
 145 150 155 160

Ser Arg Asn Thr Ile Pro Leu Ala Val Val Leu Pro Thr Glu Ile Pro
 165 170 175

 Cys Glu Asn Pro Gly Glu Ile Phe Ile Leu Arg Asp Glu Val Ile
 180 185 190

 Gly Asp Thr Val Glu Val Glu Phe Thr Ser Ser Asn Lys Arg Ile Arg
 195 200 205

 Thr Arg Pro Ala Leu Trp Asn Lys Lys Val Trp Cys Met Lys Ala Leu
 210 215 220

 Glu Phe Pro Ala Gly Ser Val His Val Asn Val Tyr Cys Asp Gly Ile
 225 230 235 240

 Val Lys Ala Thr Thr Lys Ile Lys Tyr Tyr Pro Thr Ala Lys Ala Lys
 245 250 255

 Glu Cys Leu Phe Arg Met Ala Asp Ser Gly Glu Ser Leu Cys Gln Asn
 260 265 270

 Ser Ile Glu Glu Leu Asp Gly Val Leu Thr Ser Ile Phe Lys His Glu
 275 280 285

 Ile Pro Tyr Tyr Glu Phe Gln Ser Leu Gln Thr Glu Ile Cys Ser Gln
 290 295 300

 Asn Lys Tyr Thr His Phe Lys Glu Leu Pro Thr Leu Leu His Cys Ala
 305 310 315 320

 Ala Lys Phe Gly Leu Lys Asn Leu Ala Ile His Leu Leu Gln Cys Ser
 325 330 335

 Gly Ala Thr Trp Ala Ser Lys Met Lys Asn Met Glu Gly Ser Asp Pro
 340 345 350

 Ala His Ile Ala Glu Arg His Gly His Lys Glu Leu Lys Lys Ile Phe
 355 360 365

 Glu Asp Phe Ser Ile Gln Glu Ile Asp Ile Asn Asn Glu Gln Glu Asn
 370 375 380

 Asp Tyr Glu Glu Asp Ile Ala Ser Phe Ser Thr Tyr Ile Pro Ser Thr
 385 390 395 400

 Gln Asn Pro Ala Phe His His Glu Ser Arg Lys Thr Tyr Gly Gln Ser
 405 410 415

 Ala Asp Gly Ala Glu Ala Asn Glu Met Glu Gly Glu Gly Lys Gln Asn
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 Gly Ser Gly Met Glu Thr Lys His Ser Pro Leu Glu Val Gly Ser Glu
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 Ser Ser Glu Asp Gln Tyr Asp Asp Leu Tyr Val Phe Ile Pro Gly Ala
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Leu Pro Pro Pro Arg Pro Val Ala Asn Ala Phe Gln Leu Glu Arg Pro
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 His Phe Thr Leu Pro Gly Thr Met Val Glu Gly Gln Met Glu Arg Ser
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 Gln Asn Trp Gly His Pro Gly Val Arg Gln Glu Thr Gly Asp Glu Pro
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 Glu Asp Pro Tyr Thr Phe Ala Glu Ile Asp Asp Ser Glu Tyr Asp Met
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 Ile Ile Asn Arg Pro Pro Ala Pro Thr Pro Arg Pro Thr Ser Ile Pro
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 Pro Lys Glu Glu Thr Thr Pro Tyr Ile Ala Gln Val Phe Gln Gln Lys
 595 600 605

 Thr Ala Arg Arg Gln Ser Asp Asp Asp Lys Phe Arg Gly Leu Pro Lys
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 Lys Gln Asp Arg Ala Arg Ile Glu Ser Pro Ala Phe Ser Thr Leu Arg
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 Gly Cys Leu Thr Asp Gly Gln Glu Glu Leu Ile Leu Leu Gln Glu Lys
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 Val Lys Asn Gly Lys Met Ser Met Asp Glu Ala Leu Glu Lys Phe Lys
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 His Trp Gln Met Gly Lys Ser Gly Leu Glu Met Ile Gln Gln Glu Lys
 675 680 685

 Leu Arg Gln Leu Arg Asp Cys Ile Ile Gly Lys Arg Pro Glu Glu Glu
 690 695 700

 Asn Val Tyr Asn Lys Leu Thr Ile Val His His Pro Gly Gly Lys Glu
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 Thr Ala His Asn Glu Asn Lys Phe Tyr Asn Val His Phe Ser Asn Lys
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 <213> Homo sapiens

<400> 81

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<211> 816

<212> PRT

<213> Homo sapiens

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 35 40 45
 Cys Gly Pro Ala Pro Pro Gly Asn Thr Lys Asp Ile Ile Met Ile Tyr
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 Glu Glu Asp Ala Glu Glu Trp Ala Leu Tyr Leu Thr Glu Val Phe Leu
 65 70 75 80
 His Val Val Lys Arg Glu Ala Ile Leu Leu Tyr Arg Leu Glu Asn Phe
 85 90 95
 Ser Phe Arg His Leu Glu Leu Leu Asn Leu Thr Ser Tyr Lys Cys Lys
 100 105 110
 Leu Leu Ile Leu Ser Asn Ser Leu Leu Arg Asp Leu Thr Pro Lys Lys
 115 120 125
 Cys Gln Phe Leu Glu Lys Ile Leu His Ser Pro Lys Ser Val Val Thr
 130 135 140
 Leu Leu Cys Gly Val Lys Ser Ser Asp Gln Leu Tyr Glu Leu Leu Asn
 145 150 155 160
 Ile Ser Gln Ser Arg Trp Glu Ile Ser Thr Glu Gln Glu Pro Glu Asp
 165 170 175
 Tyr Ile Ser Val Ile Gln Ser Ile Ile Phe Lys Asp Ser Glu Asp Tyr
 180 185 190
 Phe Glu Val Asn Ile Pro Thr Asp Leu Arg Ala Lys His Ser Gly Glu
 195 200 205
 Ile Ser Glu Arg Lys Glu Ile Glu Glu Leu Ser Glu Ala Ser Arg Asn
 210 215 220
 Thr Ile Pro Leu Ala Val Val Leu Pro Thr Glu Ile Pro Cys Glu Asn
 225 230 235 240
 Pro Gly Glu Ile Phe Ile Ile Leu Arg Asp Glu Val Ile Gly Asp Thr
 245 250 255
 Val Glu Val Glu Phe Thr Ser Ser Asn Lys Arg Ile Arg Thr Arg Pro
 260 265 270
 Ala Leu Trp Asn Lys Lys Val Trp Cys Met Lys Ala Leu Glu Phe Pro
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 Ala Gly Ser Val His Val Asn Val Tyr Cys Asp Gly Ile Val Lys Ala
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 Thr Thr Lys Ile Lys Tyr Tyr Pro Thr Ala Lys Ala Lys Glu Cys Leu
 305 310 315 320

Phe Arg Met Ala Asp Ser Gly Glu Ser Leu Cys Gln Asn Ser Ile Glu
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 Glu Leu Asp Gly Val Leu Thr Ser Ile Phe Lys His Glu Ile Pro Tyr
 340 345 350
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 Gly Leu Lys Asn Leu Ala Ile His Leu Leu Gln Cys Ser Gly Ala Thr
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 420 425 430
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 Glu Asp Ile Ala Ser Phe Ser Thr Tyr Ile Pro Ser Thr Gln Asn Pro
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 465 470 475 480
 Ala Glu Ala Asn Glu Met Glu Gly Glu Lys Gln Asn Gly Ser Gly
 485 490 495
 Met Glu Thr Lys His Ser Pro Leu Glu Val Gly Ser Glu Ser Ser Glu
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 Asp Gln Tyr Asp Asp Leu Tyr Val Phe Ile Pro Gly Ala Asp Pro Glu
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 Leu Pro Gly Thr Met Val Glu Gly Gln Met Glu Arg Ser Gln Asn Trp
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 Tyr Thr Phe Ala Glu Ile Asp Asp Ser Glu Tyr Asp Met Ile Leu Ala
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Arg Pro Pro Ala Pro Thr Pro Arg Pro Thr Ser Ile Pro Pro Lys Glu
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 Arg Gln Ser Asp Asp Asp Lys Phe Arg Gly Leu Pro Lys Lys Gln Asp
 675 680 685
 Arg Ala Arg Ile Glu Ser Pro Ala Phe Ser Thr Leu Arg Gly Cys Leu
 690 695 700
 Thr Asp Gly Gln Glu Glu Leu Ile Leu Leu Gln Glu Lys Val Lys Asn
 705 710 715 720
 Gly Lys Met Ser Met Asp Glu Ala Leu Glu Lys Phe Lys His Trp Gln
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 Met Gly Lys Ser Gly Leu Glu Met Ile Gln Gln Glu Lys Leu Arg Gln
 740 745 750
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 755 760 765
 Asn Lys Leu Thr Ile Val His His Pro Gly Gly Lys Glu Thr Ala His
 770 775 780
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 <211> 3544
 <212> DNA
 <213> Homo sapiens

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 <211> 770
 <212> PRT
 <213> Homo sapiens

<400> 84
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Phe Leu His Val Val Lys Arg Glu Ala Ile Leu Leu Tyr Arg Leu Glu
 35 40 45

Asn Phe Ser Phe Arg His Leu Glu Leu Leu Asn Leu Thr Ser Tyr Lys
 50 55 60

Cys Lys Leu Leu Ile Leu Ser Asn Ser Leu Leu Arg Asp Leu Thr Pro
 65 70 75 80

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Val	Thr	Leu	Leu	Cys	Gly	Val	Lys	Ser	Ser	Asp	Gln	Leu	Tyr	Glu	Leu
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Leu	Asn	Ile	Ser	Gln	Ser	Arg	Trp	Glu	Ile	Ser	Thr	Glu	Gln	Glu	Pro
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Glu	Asp	Tyr	Ile	Ser	Val	Ile	Gln	Ser	Ile	Ile	Phe	Lys	Asp	Ser	Glu
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Asp	Tyr	Phe	Glu	Val	Asn	Ile	Pro	Thr	Asp	Leu	Arg	Ala	Lys	His	Ser
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Gly	Glu	Ile	Ser	Glu	Arg	Lys	Glu	Ile	Glu	Glu	Leu	Ser	Glu	Ala	Ser
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Arg	Asn	Thr	Ile	Pro	Leu	Ala	Val	Val	Leu	Pro	Thr	Glu	Ile	Pro	Cys
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Glu	Asp	Pro	Gly	Glu	Ile	Phe	Ile	Ile	Leu	Arg	Asp	Glu	Val	Ile	Gly
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Asp	Thr	Val	Glu	Val	Glu	Phe	Thr	Ser	Ser	Asn	Lys	Arg	Ile	Arg	Thr
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Arg	Pro	Ala	Leu	Trp	Asn	Lys	Lys	Val	Trp	Cys	Met	Lys	Ala	Leu	Glu
				225			230			235			240		
Phe	Pro	Ala	Gly	Ser	Val	His	Val	Asn	Val	Tyr	Cys	Asp	Gly	Ile	Val
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Lys	Ala	Thr	Thr	Lys	Ile	Lys	Tyr	Tyr	Pro	Thr	Ala	Lys	Ala	Lys	Glu
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Cys	Leu	Phe	Arg	Met	Ala	Asp	Ser	Gly	Glu	Ser	Leu	Cys	Gln	Asn	Ser
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Ile	Glu	Glu	Leu	Asp	Gly	Val	Leu	Thr	Ser	Ile	Phe	Lys	His	Glu	Ile
				290			295				300				
Pro	Tyr	Tyr	Glu	Phe	Gln	Ser	Leu	Gln	Thr	Glu	Ile	Cys	Ser	Gln	Asn
				305			310			315			320		
Lys	Tyr	Thr	His	Phe	Lys	Glu	Leu	Pro	Thr	Leu	Leu	His	Cys	Ala	Ala
				325				330				335			
Lys	Phe	Gly	Leu	Lys	Asn	Leu	Ala	Ile	His	Leu	Leu	Gln	Cys	Ser	Gly
				340			345				350				
Ala	Thr	Trp	Ala	Ser	Lys	Met	Lys	Asn	Met	Glu	Gly	Ser	Asp	Pro	Thr
				355			360			365					
His	Ile	Ala	Glu	Arg	His	Gly	His	Lys	Glu	Leu	Lys	Lys	Ile	Phe	Glu
				370			375				380				
Asp	Phe	Ser	Ile	Gln	Glu	Ile	Asp	Ile	Asn	Asn	Glu	Gln	Glu	Asn	Asp
				385			390			395			400		

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 405 410 415

 Asn Pro Ala Phe His His Glu Ser Arg Lys Thr Tyr Gly Gln Ser Ala
 420 425 430

 Asp Gly Ala Glu Ala Asn Glu Met Glu Gly Glu Gly Lys Gln Asn Gly
 435 440 445

 Ser Gly Met Glu Thr Lys His Ser Pro Leu Glu Val Gly Ser Glu Ser
 450 455 460

 Ser Glu Asp Gln Tyr Asp Asp Leu Tyr Val Phe Ile Pro Gly Ala Asp
 465 470 475 480

 Pro Glu Asn Asn Ser Gln Glu Pro Leu Met Ser Ser Arg Pro Pro Leu
 485 490 495

 Pro Pro Pro Arg Pro Val Ala Asn Ala Phe Gln Leu Glu Arg Pro His
 500 505 510

 Phe Thr Leu Pro Gly Thr Met Val Glu Gly Gln Met Glu Arg Ser Gln
 515 520 525

 Asn Trp Gly His Pro Gly Val Arg Gln Glu Thr Gly Asp Glu Pro Lys
 530 535 540

 Gly Glu Lys Glu Lys Lys Glu Glu Lys Glu Gln Glu Glu Glu Glu
 545 550 555 560

 Asp Pro Tyr Thr Phe Ala Glu Ile Asp Asp Ser Glu Tyr Asp Met Ile
 565 570 575

 Leu Ala Asn Leu Ser Ile Lys Lys Lys Thr Gly Ser Arg Ser Phe Ile
 580 585 590

 Ile Asn Arg Pro Pro Ala Pro Thr Pro Arg Pro Thr Ser Ile Pro Pro
 595 600 605

 Lys Glu Glu Thr Thr Pro Tyr Ile Ala Gln Val Phe Gln Gln Lys Thr
 610 615 620

 Ala Arg Arg Gln Ser Asp Asp Asp Lys Phe Arg Gly Leu Pro Lys Lys
 625 630 635 640

 Gln Asp Arg Ala Arg Ile Glu Ser Pro Ala Phe Ser Thr Leu Arg Gly
 645 650 655

 Cys Leu Thr Asp Gly Gln Glu Glu Leu Ile Leu Leu Gln Glu Lys Val
 660 665 670

 Lys Asn Gly Lys Met Ser Met Asp Glu Ala Leu Glu Lys Phe Lys His
 675 680 685

 Trp Gln Met Gly Lys Ser Gly Leu Glu Met Ile Gln Gln Glu Lys Leu
 690 695 700

 Arg Gln Leu Arg Asp Cys Ile Ile Gly Lys Arg Pro Glu Glu Glu Asn
 705 710 715 720

Val Tyr Asn Lys Leu Thr Ile Val His His Pro Gly Gly Lys Glu Thr
725 730 735

Ala His Asn Glu Asn Lys Phe Tyr Asn Val His Phe Ser Asn Lys Leu
740 745 750

Pro Ala Arg Pro Gln Val Glu Lys Glu Phe Gly Phe Cys Cys Lys Lys
755 760 765

Asp His
770

<210> 85

<211> 564

<212> DNA

<213> Homo sapiens

<400> 85

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<211> 5024

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<213> Homo sapiens

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<211> 305
<212> PRT
<213> Homo sapiens

<400> 87
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35 40 45

Gln Asn Thr Thr Glu Val Tyr Val Lys Trp Lys Phe Lys Gly Arg Asp
50 55 60

Ile Tyr Thr Phe Asp Gly Ala Leu Asn Lys Ser Thr Val Pro Thr Asp
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Phe Ser Ser Ala Lys Ile Glu Val Ser Gln Leu Leu Lys Gly Asp Ala
85 90 95

Ser Leu Lys Met Asp Lys Ser Asp Ala Val Ser His Thr Gly Asn Tyr
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Thr Cys Glu Val Thr Glu Leu Thr Arg Glu Gly Glu Thr Ile Ile Glu
115 120 125

Leu Lys Tyr Arg Val Val Ser Trp Phe Ser Pro Asn Glu Asn Ile Leu
130 135 140

Ile Val Ile Phe Pro Ile Phe Ala Ile Leu Leu Phe Trp Gly Gln Phe
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Gly Ile Lys Thr Leu Lys Tyr Arg Ser Gly Gly Met Asp Glu Lys Thr
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Ile Ala Leu Leu Val Ala Gly Leu Val Ile Thr Val Ile Val Ile Val
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Gly Ala Ile Leu Phe Val Pro Gly Glu Tyr Ser Leu Lys Asn Ala Thr
195 200 205

Gly Leu Gly Leu Ile Val Thr Ser Thr Gly Ile Leu Ile Leu Leu His
210 215 220

Tyr Tyr Val Phe Ser Thr Ala Ile Gly Leu Thr Ser Phe Val Ile Ala
225 230 235 240

Ile Leu Val Ile Gln Val Ile Ala Tyr Ile Leu Ala Val Val Gly Leu
245 250 255

Ser Leu Cys Ile Ala Ala Cys Ile Pro Met His Gly Pro Leu Leu Ile
260 265 270

Ser Gly Leu Ser Ile Leu Ala Leu Ala Gln Leu Leu Gly Leu Val Tyr
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Asn
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<212> DNA
<213> Homo sapiens

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<213> *Homo sapiens*

<210> 90
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<212> DNA
<213> *Homo sapiens*

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<212> DNA
<213> Homo sapiens

<400> 93

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gtttgc	cc	ctc	tttgc	tttgc	tttgc	4260
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ttttgc	gtt	tttgc	tttgc	tttgc	tttgc	4500
actactgt	gtt	tttgc	tttgc	tttgc	tttgc	4560
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aaaatttctg	atcccatttc	tgatggatgt	gtcacaccc	ttctgtcaaa	ataaaaatgtc	6360
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<210> 94
<211> 1364
<212> DNA
<213> Homo

<400> 94
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tcatctaaaa ttgggtcaag gggagggct ttcttggtcc ctccttttgt tcaaggaaa 180
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atttctagat gtcaaggcat cttagatga tggggtgagg actgcagtgg ccatcccaga 360
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ccataagaag gtgctatagt ttttataaaa tatctttcta cagtcatccc cctttttga 780
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<210> 95
<211> 411
<212> DNA
<213> Homo sapiens

<400> 95
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gcacatttat gtgttggtga atgccaggga ttcagcttag gtctgattgc tcaccacaca 180
qaaaqccaat caactqagaca acaaqtactq ccaqqaagaa aggctttatt gctggtgatg 240

ccagccagga tatgggagac aagtctaaaa tctgtctctg taaccaataa agttaggagt 300
ttatgttagga gttgctcaac aggcatagg tagttgaatc agggttctgg caccttgctg 360
ttaggatgca gcgatctgga aatcttcagc tttctgatac tatctggag g 411

<210> 96
<211> 1632
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1)..(1632)
<223> n = g, a, c or t

<400> 96
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tctttatgca ttttttttaa tttaaatgt gggtaggaa tctaactttt ttcaaacaca 180
tataaatgtg cactactatt tatttaataa gtctgttctt ttccctttta ttattatgct 240
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attaattaaa attatttgca taaaatgctt aagacagggc ctgaaatgac attgagtcct 1560
aaaaaaaaaaa attatttatttca tcatccttc aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaana 1620
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<210> 97
<211> 2378
<212> DNA
<213> Homo sapiens

<400> 97
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gccagtcctcag ggagaggaca gagccaatgg actgggtgt actgtaaacag ccctgctggc 180
gagaggggacc agggcaccgt cctccaggaa gcccattctg caagtcgggc cagaggtgcc 240
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cagttggaaag cagccatcc agcctgcggaa gctgtgggg caggttaagg gcaagagata 480
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 acattactcttttcttgc caaaaaaaaaaaaaaaa 2378

<210> 98
 <211> 313
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1)..(313)
 <223> n = g, a, c or t

<400> 98
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 tataaactat taggttggtg caaaactaat tgggtttt gcaattgaa tggcattgaa 180
 ataaaagtgt aaagaaatct ataccagatg tagtaacagt gtttgggttc tgggaggtt 240
 gattacaggg agcatttgcattttgtatgtc ngtatttcta tantgttga attgtttaga 300
 atgaatctgt ntt 313

<210> 99
 <211> 317
 <212> DNA
 <213> Homo sapiens

<400> 99
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gaaggcacag caggtggcca ggaggcaaca ggagcgaaag gctgtgacaa agaggagccc 240
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<210> 100
 <211> 1968
 <212> DNA
 <213> Homo sapiens

<400> 100

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 gcccacttcc ttccctgaa gaaatatctg tgaaccttct ttctgttcag tcctaaaattt 1920
 cgaaaataaag tgagactatg gttcacctgt aaaaaaaaaa aaggaatt 1968

<210> 101
 <211> 486
 <212> PRT
 <213> Homo sapiens

<400> 101
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Gln Gly Asp Asp Trp Asp Thr Asp Pro Asp Phe Val Asn Asp Ile Ser
 20 25 30

Glu Lys Glu Glu Gln Arg Trp Gly Ala Lys Thr Ile Glu Gly Ser Gly Arg
 35 40 45

Thr Glu His Ile Asn Ile His Gln Leu Arg Asn Lys Val Ser Glu Glu
 50 55 60

His Asp Val Leu Arg Lys Lys Glu Met Glu Ser Gly Pro Lys Ala Ser
 65 70 75 80

His Gly Tyr Gly Gly Arg Phe Gly Val Glu Arg Asp Arg Met Asp Lys
 85 90 95

Ser Ala Val Gly His Glu Tyr Val Ala Glu Val Glu Lys His Ser Ser
 100 105 110

Gln Thr Asp Ala Ala Lys Gly Phe Gly Gly Lys Tyr Gly Val Glu Arg
 115 120 125

Asp Arg Ala Asp Lys Ser Ala Val Gly Phe Asp Tyr Lys Gly Glu Val
 130 135 140

Glu Lys His Thr Ser Gln Lys Asp Tyr Ser Arg Gly Phe Gly Gly Arg
 145 150 155 160

Tyr Gly Val Glu Lys Asp Lys Trp Asp Lys Ala Ala Leu Gly Tyr Asp
 165 170 175

Tyr Lys Gly Glu Thr Glu Lys His Glu Ser Gln Arg Asp Tyr Ala Lys
 180 185 190

Gly Phe Gly Gly Gln Tyr Gly Ile Gln Lys Asp Arg Val Asp Lys Ser
 195 200 205

Ala Val Gly Phe Asn Glu Met Glu Ala Pro Thr Thr Ala Tyr Lys Lys
 210 215 220

Thr Thr Pro Ile Glu Ala Ala Ser Ser Gly Ala Arg Gly Leu Lys Ala
 225 230 235 240

Lys Phe Glu Ser Met Ala Glu Glu Lys Arg Lys Arg Glu Glu Glu
 245 250 255

Lys Ala Gln Gln Val Ala Arg Arg Gln Gln Glu Arg Lys Ala Val Thr
 260 265 270

Lys Arg Ser Pro Glu Ala Pro Gln Pro Val Ile Ala Met Glu Glu Pro
 275 280 285

Ala Val Pro Ala Pro Leu Pro Lys Lys Ile Ser Ser Glu Ala Trp Pro
 290 295 300

Pro Val Gly Thr Pro Pro Ser Ser Glu Ser Glu Pro Val Arg Thr Ser
 305 310 315 320

Arg Glu His Pro Val Pro Leu Leu Pro Ile Arg Gln Thr Leu Pro Glu
 325 330 335

Asp Asn Glu Glu Pro Pro Ala Leu Pro Pro Arg Thr Leu Glu Gly Leu
 340 345 350

Gln Val Glu Glu Glu Pro Val Tyr Glu Ala Glu Pro Glu Pro Glu Pro
 355 360 365

Glu	Pro	Glu	Pro	Glu	Pro	Glu	Asn	Asp	Tyr	Glu	Asp	Val	Glu	Glu	Met
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														380	
Asp	Arg	His	Glu	Gln	Glu	Asp	Glu	Pro	Glu	Gly	Asp	Tyr	Glu	Glu	Val
385															
														390	395
Leu	Glu	Pro	Glu	Asp	Ser	Ser	Phe	Ser	Ser	Ala	Leu	Ala	Gly	Ser	Ser
														405	410
Gly	Cys	Pro	Ala	Gly	Ala	Gly	Ala	Val	Ala	Leu	Gly	Ile	Ser		
														420	425
Ala	Val	Ala	Leu	Tyr	Asp	Tyr	Gln	Gly	Glu	Gly	Ser	Asp	Glu	Leu	Ser
														435	440
Phe	Asp	Pro	Asp	Asp	Val	Ile	Thr	Asp	Ile	Glu	Met	Val	Asp	Glu	Gly
														450	455
Trp	Trp	Arg	Gly	Arg	Cys	His	Gly	His	Phe	Gly	Leu	Phe	Pro	Ala	Asn
														465	470
Tyr	Val	Lys	Leu	Leu	Glu										
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<210> 102

<211> 96

<212> DNA

<213> Homo sapiens

<400> 102

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<210> 103

<211> 349

<212> DNA

<213> Homo sapiens

<400> 103

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ccacggcaag	gacatcccc	tcgaactcag	gcagctcctt	tttgcagcct	ggctcgagtt	180
ggctcagcac	aaaaggtaaa	aagatgcaga	gaccccgacc	tccgatgaac	ctcctctgcg	240
ccaaccgc	gtccgatttg	aatttcttca	gcacgcgccc	cctgactctc	tccagcctct	300
gggcagcctg	gtcacagttg	agggccgtcg	tcagacactg	gtcagccag		349

<210> 104

<211> 116

<212> PRT

<213> Homo sapiens

<400> 104

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1														
														10
														15

Gln	Arg	Leu	Glu	Arg	Val	Arg	Gly	Arg	Val	Leu	Lys	Lys	Phe	Lys	Ser
														20	25
															30

Asp Ser Gly Leu Ala Gln Arg Arg Phe Ile Arg Gly Trp Gly Leu Cys
35 40 45

Ile Phe Leu Pro Phe Val Leu Ser Gln Leu Glu Pro Gly Cys Lys Lys
50 55 60

Glu Leu Pro Glu Phe Glu Gly Asp Val Leu Ala Val Gly Ser Gln Ala
65 70 75 80

Leu Thr Thr Glu Gly Ile Tyr Glu Asp Val Ile Arg Gly Cys Leu Leu
85 90 95

Gln Arg Ile Asp Gln Glu Leu Lys Lys Thr Leu Gly Ala Asn Asp Val
100 105 110

Ser Cys Thr Leu
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<400> 105

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<211> 5107

<212> DNA

<213> Homo sapiens

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<212> PRT
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<400> 107
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35 40 45

Tyr Arg Gly Gln Leu Ala Ala Ser Val Leu Arg Gln Ile Ser Arg Glu
50 55 60

Leu Gly Pro Gln Glu Pro Thr Gly Ser Gln Leu Leu Arg Ser Lys Lys
65 70 75 80

Leu Pro Arg Val Arg Glu His Arg Gly Pro Leu Thr Gln Leu Arg Gly
85 90 95

His Pro Pro Arg Trp Gln Pro Ile Phe Cys Val Leu Arg Gly Asp Gly
100 105 110

Arg Leu Glu Trp Phe Ser His Lys Glu Glu Tyr Glu Asn Gly Gly His
115 120 125

Cys Leu Gly Ser Thr Ala Leu Thr Gly Tyr Thr Leu Leu Thr Ser Gln
130 135 140

Arg Glu Tyr Leu Arg Leu Leu Asp Ala Leu Cys Pro Glu Ser Leu Gly
145 150 155 160

Asp His Thr Gln Glu Glu Pro Asp Ser Leu Leu Glu Val Pro Val Ser
165 170 175

Phe Pro Leu Phe Leu Gln His Pro Phe Arg Arg His Leu Cys Phe Ser
180 185 190

Ala Ala Thr Arg Glu Ala Gln His Ala Trp Arg Leu Ala Leu Gln Gly
195 200 205

Gly Ile Arg Leu Gln Gly Thr Val Leu Gln Arg Ser Gln Ala Pro Ala
210 215 220

Ala Arg Ala Phe Leu Asp Ala Val Arg Leu Tyr Arg Gln His Gln Gly
225 230 235 240

His Phe Gly Asp Asp Asp Val Thr Leu Gly Ser Asp Ala Glu Val Leu
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 Glu Lys Thr Ile Arg Pro Asp Val Asp Gln Leu Leu Arg Gln Arg Ala
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 Arg Val Ala Gly Arg Leu Arg Thr Asp Ile Arg Gly Pro Leu Glu Ser
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 Cys Leu Arg Arg Glu Val Asp Pro Gln Leu Pro Arg Val Val Gln Thr
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 Ala Gln Gly Met Asp Arg Leu Ser His Arg Leu Arg Gln Ser Pro Ser
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 Gly Arg Leu Gly Gln Leu Ala Ala Pro Phe Gly Phe Leu Gly Met Gln
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<212> DNA

<213> Homo sapiens

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<210> 111
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<212> DNA
<213> *Homo sapiens*

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<211> 1750
<212> DNA
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<210> 114
<211> 547
<212> PRT
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<400> 114
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 35 40 45
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 50 55 60
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 65 70 75 80
 Ala Ala Phe Asn Leu Ser Asn Val Thr Gly Asn Ser Arg Ile Leu Cys
 85 90 95
 Ser Val Tyr Cys Asn Gly Ser Gln Ile Thr Gly Ser Ser Asn Ile Thr
 100 105 110
 Val Tyr Gly Leu Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Pro Trp
 115 120 125
 Gln Pro Val Gly Gln Asn Phe Thr Leu Arg Cys Gln Val Glu Gly
 130 135 140
 Ser Pro Arg Thr Ser Leu Thr Val Val Leu Leu Arg Trp Glu Glu
 145 150 155 160
 Leu Ser Arg Gln Pro Ala Val Glu Pro Ala Glu Val Thr Ala Thr
 165 170 175
 Val Leu Ala Ser Arg Asp Asp His Gly Ala Pro Phe Ser Cys Arg Thr
 180 185 190
 Glu Leu Asp Met Gln Pro Gln Gly Leu Gly Leu Phe Val Asn Thr Ser
 195 200 205
 Ala Pro Arg Gln Leu Arg Thr Phe Val Leu Pro Val Thr Pro Pro Arg
 210 215 220
 Leu Val Ala Pro Arg Phe Leu Glu Val Glu Thr Ser Trp Pro Val Asp
 225 230 235 240
 Cys Thr Leu Asp Gly Leu Phe Pro Ala Ser Glu Ala Gln Val Tyr Leu
 245 250 255
 Ala Leu Gly Asp Gln Met Leu Asn Ala Thr Val Met Asn His Gly Asp
 260 265 270
 Thr Leu Thr Ala Thr Ala Thr Ala Arg Ala Asp Gln Glu Gly
 275 280 285
 Ala Arg Glu Ile Val Cys Asn Val Thr Leu Gly Gly Glu Arg Arg Glu
 290 295 300
 Ala Arg Glu Asn Leu Thr Val Phe Ser Phe Leu Gly Pro Ile Val Asn
 305 310 315 320

Leu Ser Glu Pro Thr Ala His Glu Gly Ser Thr Val Thr Val Ser Cys
 325 330 335

 Met Ala Gly Ala Arg Val Gln Val Thr Leu Asp Gly Val Pro Ala Ala
 340 345 350

 Ala Pro Gly Gln Pro Ala Gln Leu Gln Leu Asn Ala Thr Glu Ser Asp
 355 360 365

 Asp Gly Arg Ser Phe Phe Cys Ser Ala Thr Leu Glu Val Asp Gly Glu
 370 375 380

 Phe Leu His Arg Asn Ser Ser Val Gln Leu Arg Val Leu Tyr Gly Pro
 385 390 395 400

 Lys Ile Asp Arg Ala Thr Cys Pro Gln His Leu Lys Trp Lys Asp Lys
 405 410 415

 Thr Arg His Val Leu Gln Cys Gln Ala Arg Gly Asn Pro Tyr Pro Glu
 420 425 430

 Leu Arg Cys Leu Lys Glu Gly Ser Ser Arg Glu Val Pro Val Gly Ile
 435 440 445

 Pro Phe Phe Val Asn Val Thr His Asn Gly Thr Tyr Gln Cys Gln Ala
 450 455 460

 Ser Ser Ser Arg Gly Lys Tyr Thr Leu Val Val Val Met Asp Ile Glu
 465 470 475 480

 Ala Gly Ser Ser His Phe Val Pro Val Phe Val Ala Val Leu Leu Thr
 485 490 495

 Leu Gly Val Val Thr Ile Val Leu Ala Leu Met Tyr Val Phe Arg Glu
 500 505 510

 His Gln Arg Ser Gly Ser Tyr His Val Arg Glu Glu Ser Thr Tyr Leu
 515 520 525

 Pro Leu Thr Ser Met Gln Pro Thr Glu Ala Met Gly Glu Glu Pro Ser
 530 535 540

 Arg Ala Glu
 545

<210> 115
 <211> 275
 <212> DNA
 <213> Homo sapiens

<400> 115
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 cgatactcag gccatgaagt acttgcata cctgctgtac cctctctgtg tcgggggtgc 120
 tgtctattca ctccctgaata tcaaataataa gagctgtac tcctggtaa tcaacagctt 180
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<210> 116
<211> 2040
<212> DNA
<213> Homo sapiens

<400> 116

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cggggagtct gatacacacg agatcgaggg ggagaagaag ccgacgagtg ccctggatga 480
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gggggtctgtt ggatttccat ttccagggtt tttctaagtg ctcccttatgt gaattcaaa 1980
cacgtatgga attcattccg catggactct gggatcaaag gctctttcctt cttttgttt 2040

<210> 117
<211> 538
<212> PRT
<213> Homo sapiens

<400> 117

Met	Trp	Ser	Gly	Arg	Ser	Ser	Phe	Thr	Ser	Leu	Val	Val	Gly	Val	Phe
1							5			10				15	

Val Val Tyr Val Val His Thr Cys Trp Val Met Tyr Gly Ile Val Tyr

					20				25				30		
--	--	--	--	--	----	--	--	--	----	--	--	--	----	--	--

Thr Arg Pro Cys Ser Gly Asp Ala Asn Cys Ile Gln Pro Tyr Leu Ala

					35				40				45		
--	--	--	--	--	----	--	--	--	----	--	--	--	----	--	--

Arg Arg Pro Lys Leu Gln Leu Ser Val Tyr Thr Thr Thr Arg Ser His

					50				55				60		
--	--	--	--	--	----	--	--	--	----	--	--	--	----	--	--

Leu Gly Ala Glu Asn Asn Ile Asp Leu Val Leu Asn Val Glu Asp Phe
 65 70 75 80

Asp Val Glu Ser Lys Phe Glu Arg Thr Val Asn Val Ser Val Pro Lys
 85 90 95

Lys Thr Arg Asn Asn Gly Thr Leu Tyr Ala Tyr Ile Phe Leu His His
 100 105 110

Ala Gly Val Leu Pro Trp His Asp Gly Lys Gln Val His Leu Val Ser
 115 120 125

Pro Leu Thr Thr Tyr Met Val Pro Lys Pro Glu Glu Ile Asn Leu Leu
 130 135 140

Thr Gly Glu Ser Asp Thr Gln Gln Ile Glu Ala Glu Lys Lys Pro Thr
 145 150 155 160

Ser Ala Leu Asp Glu Pro Val Ser His Trp Arg Pro Arg Leu Ala Leu
 165 170 175

Asn Val Met Ala Asp Asn Phe Val Phe Asp Gly Ser Ser Leu Pro Ala
 180 185 190

Asp Val His Arg Tyr Met Lys Met Ile Gln Leu Gly Lys Thr Val His
 195 200 205

Tyr Leu Pro Ile Leu Phe Ile Asp Gln Leu Ser Asn Arg Val Lys Asp
 210 215 220

Leu Met Val Ile Asn Arg Ser Thr Thr Glu Leu Pro Leu Thr Val Ser
 225 230 235 240

Tyr Asp Lys Val Ser Leu Gly Arg Leu Arg Phe Trp Ile His Met Gln
 245 250 255

Asp Ala Val Tyr Ser Leu Gln Gln Phe Gly Phe Ser Glu Lys Asp Ala
 260 265 270

Asp Glu Val Lys Gly Ile Phe Val Asp Thr Asn Leu Tyr Phe Leu Ala
 275 280 285

Leu Thr Phe Phe Val Ala Ala Phe His Leu Leu Phe Asp Phe Leu Ala
 290 295 300

Phe Lys Asn Asp Ile Ser Phe Trp Lys Lys Lys Ser Met Ile Gly
 305 310 315 320

Met Ser Thr Lys Ala Val Leu Trp Arg Cys Phe Ser Thr Val Val Ile
 325 330 335

Phe Leu Phe Leu Leu Asp Glu Gln Thr Ser Leu Leu Val Leu Val Pro
 340 345 350

Ala Gly Val Gly Ala Ala Ile Glu Leu Trp Lys Val Lys Lys Ala Leu
 355 360 365

Lys Met Thr Ile Phe Trp Arg Gly Leu Met Pro Glu Phe Gln Phe Gly
 370 375 380

Thr Tyr Ser Glu Ser Glu Arg Lys Thr Glu Glu Tyr Asp Thr Gln Ala
 385 390 395 400

 Met Lys Tyr Leu Ser Tyr Leu Leu Tyr Pro Leu Cys Val Gly Gly Ala
 405 410 415

 Val Tyr Ser Leu Leu Asn Ile Lys Tyr Lys Ser Trp Tyr Ser Trp Leu
 420 425 430

 Ile Asn Ser Phe Val Asn Gly Val Tyr Ala Phe Gly Phe Leu Phe Met
 435 440 445

 Leu Pro Gln Leu Phe Val Asn Tyr Lys Leu Lys Ser Val Ala His Leu
 450 455 460

 Pro Trp Lys Ala Phe Thr Tyr Lys Ala Phe Asn Thr Phe Ile Asp Asp
 465 470 475 480

 Val Phe Ala Phe Ile Ile Thr Met Pro Thr Ser His Arg Leu Ala Cys
 485 490 495

 Phe Arg Asp Asp Val Val Phe Leu Val Tyr Leu Tyr Gln Arg Trp Leu
 500 505 510

 Tyr Pro Val Asp Lys Arg Arg Val Asn Glu Phe Gly Glu Ser Tyr Glu
 515 520 525

 Glu Lys Ala Thr Arg Ala Pro His Thr Asp
 530 535

<210> 118
 <211> 4217
 <212> DNA
 <213> Homo sapiens

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 gcacaagaag cccttccttg ccaaataactt cccctttatg gacctgaagc tccgagcagc 180
 ctccccgatc attacattgg tggcccttga tgaagccctt gacaactaca ccatcacatt 240
 cctcatccgc ggtgtggcca tcggccagac cagtctaact gcaagtgtga ccaataaagc 300
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 gttctatgtt atttttt 4217

<210> 119
 <211> 923
 <212> PRT
 <213> Homo sapiens

<400> 119
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Leu Tyr Ile Arg Val Val Asp Lys Val Glu Ile Gly Lys Thr Val Lys
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Ala Tyr Val Arg Val Leu Asp Leu His Lys Lys Pro Phe Leu Ala Lys
 35 40 45

Tyr Phe Pro Phe Met Asp Leu Lys Leu Arg Ala Ala Ser Pro Ile Ile
 50 55 60

Thr Leu Val Ala Leu Asp Glu Ala Leu Asp Asn Tyr Thr Ile Thr Phe
 65 70 75 80

Leu Ile Arg Gly Val Ala Ile Gly Gln Thr Ser Leu Thr Ala Ser Val
 85 90 95

Thr Asn Lys Ala Gly Gln Arg Ile Asn Ser Ala Pro Gln Gln Ile Glu
 100 105 110

Val Phe Pro Pro Phe Arg Leu Met Pro Arg Lys Val Thr Leu Leu Ile
 115 120 125

Gly Ala Thr Met Gln Val Thr Ser Glu Gly Gly Pro Gln Pro Gln Ser
 130 135 140

Asn Ile Leu Phe Ser Ile Ser Asn Glu Ser Val Ala Leu Val Ser Ala
 145 150 155 160

Ala Gly Leu Val Gln Gly Leu Ala Ile Gly Asn Gly Thr Val Ser Gly
 165 170 175

Leu Val Gln Ala Val Asp Ala Glu Thr Gly Lys Val Val Ile Ile Ser
 180 185 190

Gln Asp Leu Val Gln Val Glu Val Leu Leu Leu Arg Ala Val Arg Ile
 195 200 205

Arg Ala Pro Ile Met Arg Met Arg Thr Gly Thr Gln Met Pro Ile Tyr
 210 215 220

Val Thr Gly Ile Thr Asn His Gln Asn Pro Phe Ser Phe Gly Asn Ala
 225 230 235 240

Val Pro Gly Leu Thr Phe His Trp Ser Val Thr Lys Arg Asp Val Leu
 245 250 255

Asp Leu Arg Gly Arg His His Glu Ala Ser Ile Arg Leu Pro Ser Gln
 260 265 270

Tyr Asn Phe Ala Met Asn Val Leu Gly Arg Val Lys Gly Arg Thr Gly
 275 280 285

Leu Arg Val Val Val Lys Ala Val Asp Pro Thr Ser Gly Gln Leu Tyr
 290 295 300

Gly Leu Ala Arg Glu Leu Ser Asp Glu Ile Gln Val Gln Val Phe Glu
 305 310 315 320

Lys Leu Gln Leu Leu Asn Pro Glu Ile Glu Ala Glu Gln Ile Leu Met
 325 330 335

Ser Pro Asn Ser Tyr Ile Lys Leu Gln Thr Asn Arg Asp Gly Ala Ala
 340 345 350

Ser Leu Ser Tyr Arg Val Leu Asp Gly Pro Glu Lys Val Pro Val Val
 355 360 365
 His Val Asp Glu Lys Gly Phe Leu Ala Ser Gly Ser Met Ile Gly Thr
 370 375 380
 Ser Thr Ile Glu Val Ile Ala Gln Glu Pro Phe Gly Ala Asn Gln Thr
 385 390 395 400
 Ile Ile Val Ala Val Lys Val Ser Pro Val Ser Tyr Leu Arg Val Ser
 405 410 415
 Met Ser Pro Val Leu His Thr Gln Asn Lys Glu Ala Leu Val Ala Val
 420 425 430
 Pro Leu Gly Met Thr Val Thr Phe Thr Val His Phe His Asp Asn Ser
 435 440 445
 Gly Asp Val Phe His Ala His Ser Ser Val Leu Asn Phe Ala Thr Asn
 450 455 460
 Arg Asp Asp Phe Val Gln Ile Gly Lys Gly Pro Thr Asn Asn Thr Cys
 465 470 475 480
 Val Val Arg Thr Val Ser Val Gly Leu Thr Leu Leu Arg Val Trp Asp
 485 490 495
 Ala Glu His Pro Gly Leu Ser Asp Phe Met Pro Leu Pro Val Leu Gln
 500 505 510
 Ala Ile Ser Pro Glu Leu Ser Gly Ala Met Val Val Gly Asp Val Leu
 515 520 525
 Cys Leu Ala Thr Val Leu Thr Ser Leu Glu Gly Leu Ser Gly Thr Trp
 530 535 540
 Ser Ser Ser Ala Asn Ser Ile Leu His Ile Asp Pro Lys Thr Gly Val
 545 550 555 560
 Ala Val Ala Arg Ala Val Gly Ser Val Thr Val Tyr Tyr Glu Val Ala
 565 570 575
 Gly His Leu Arg Thr Tyr Lys Glu Val Val Val Ser Val Pro Gln Arg
 580 585 590
 Ile Met Ala Arg His Leu His Pro Ile Gln Thr Ser Phe Gln Glu Ala
 595 600 605
 Thr Ala Ser Lys Val Ile Val Ala Val Gly Asp Arg Ser Ser Asn Leu
 610 615 620
 Arg Gly Glu Cys Thr Pro Thr Gln Arg Glu Val Ile Gln Ala Leu His
 625 630 635 640
 Pro Glu Thr Leu Ile Ser Cys Gln Ser Gln Phe Lys Pro Ala Val Phe
 645 650 655
 Asp Phe Pro Ser Gln Asp Val Phe Thr Val Glu Pro Gln Phe Asp Thr
 660 665 670

Ala Leu Gly Gln Tyr Phe Cys Ser Ile Thr Met His Arg Leu Thr Asp
 675 680 685
 Lys Gln Arg Lys His Leu Ser Met Lys Lys Thr Ala Leu Val Val Ser
 690 695 700
 Ala Ser Leu Ser Ser His Phe Ser Thr Glu Gln Val Gly Ala Glu
 705 710 715 720
 Val Pro Phe Ser Pro Gly Leu Phe Ala Asp Gln Ala Glu Ile Leu Leu
 725 730 735
 Ser Asn His Tyr Thr Ser Ser Glu Ile Arg Val Phe Gly Ala Pro Glu
 740 745 750
 Val Leu Glu Asn Leu Glu Val Lys Ser Gly Ser Pro Ala Val Leu Ala
 755 760 765
 Phe Ala Lys Glu Lys Ser Phe Gly Trp Pro Ser Phe Ile Thr Tyr Thr
 770 775 780
 Val Gly Val Ser Asp Pro Ala Ala Gly Ser Gln Gly Pro Leu Ser Thr
 785 790 795 800
 Thr Leu Thr Phe Ser Ser Pro Val Thr Asn Gln Ala Ile Ala Ile Pro
 805 810 815
 Val Thr Val Ala Phe Val Met Asp Arg Arg Gly Pro Gly Pro Tyr Gly
 820 825 830
 Ala Ser Leu Phe Gln His Phe Leu Asp Ser Tyr Gln Val Met Phe Phe
 835 840 845
 Thr Leu Phe Ala Leu Leu Ala Gly Thr Ala Val Met Ile Ile Ala Tyr
 850 855 860
 His Thr Val Cys Thr Pro Arg Asp Leu Ala Val Pro Ala Ala Leu Thr
 865 870 875 880
 Pro Arg Ala Ser Pro Gly His Ser Pro His Tyr Phe Ala Ala Ser Ser
 885 890 895
 Pro Thr Ser Pro Asn Ala Leu Pro Pro Ala Arg Lys Ala Ser Pro Pro
 900 905 910
 Ser Gly Leu Trp Ser Pro Ala Tyr Ala Ser His
 915 920

<210> 120
 <211> 1270
 <212> PRT
 <213> Homo sapiens

<400> 120
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Met Thr Ser Gly Gly Asp Ala Ala Met Phe Arg Asp Gly Lys Glu Pro
 20 25 30

Gln Pro Ser Ala Glu Ala Ala Ala Pro Ser Leu Ala Asn Ile Ser
 35 40 45

Cys Phe Thr Gln Lys Leu Val Glu Lys Leu Tyr Ser Gly Met Phe Ser
 50 55 60

Ala Asp Pro Arg His Ile Leu Leu Phe Ile Leu Glu His Ile Met Val
 65 70 75 80

Val Ile Glu Thr Ala Ser Ser Gln Arg Asp Thr Val Leu Ser Thr Leu
 85 90 95

Tyr Ser Ser Leu Asn Lys Val Ile Leu Tyr Cys Leu Ser Lys Pro Gln
 100 105 110

Gln Ser Leu Ser Glu Cys Leu Gly Leu Leu Ser Ile Leu Gly Phe Leu
 115 120 125

Gln Glu His Trp Asp Val Val Phe Ala Thr Tyr Asn Ser Asn Ile Ser
 130 135 140

Phe Leu Leu Cys Leu Met His Cys Leu Leu Leu Leu Asn Glu Arg Ser
 145 150 155 160

Tyr Pro Glu Gly Phe Gly Leu Glu Pro Lys Pro Arg Met Ser Thr Tyr
 165 170 175

His Gln Val Phe Leu Ser Pro Asn Glu Asp Val Lys Glu Lys Arg Glu
 180 185 190

Asp Leu Pro Ser Leu Ser Asp Val Gln His Asn Ile Gln Lys Thr Val
 195 200 205

Gln Thr Leu Trp Gln Gln Leu Val Ala Gln Arg Gln Gln Thr Leu Glu
 210 215 220

Asp Ala Phe Lys Ile Asp Leu Ser Val Lys Pro Gly Glu Arg Glu Val
 225 230 235 240

Lys Ile Glu Glu Val Thr Pro Leu Trp Glu Glu Thr Met Leu Lys Ala
 245 250 255

Trp Gln His Tyr Leu Ala Ser Glu Lys Ser Leu Ala Ser Arg Ser
 260 265 270

Asn Val Ala His His Ser Lys Val Thr Leu Trp Ser Gly Ser Leu Ser
 275 280 285

Ser Ala Met Lys Leu Met Pro Gly Arg Gln Ala Lys Asp Pro Glu Cys
 290 295 300

Lys Thr Glu Asp Phe Val Ser Cys Ile Glu Asn Tyr Arg Arg Arg Gly
 305 310 315 320

Gln Glu Leu Tyr Ala Ser Leu Tyr Lys Asp His Val Gln Arg Arg Lys
 325 330 335

Cys Gly Asn Ile Lys Ala Ala Asn Ala Trp Ala Arg Ile Gln Glu Gln
 340 345 350

Leu Phe Gly Glu Leu Gly Leu Trp Ser Gln Gly Glu Glu Thr Lys Pro
 355 360 365

 Cys Ser Pro Trp Glu Leu Asp Trp Arg Glu Gly Pro Ala Arg Met Arg
 370 375 380

 Lys Arg Ile Lys Arg Leu Ser Pro Leu Glu Ala Leu Ser Ser Gly Arg
 385 390 395 400

 His Lys Glu Ser Gln Asp Lys Asn Asp His Ile Ser Gln Thr Asn Ala
 405 410 415

 Glu Asn Gln Asp Glu Leu Thr Leu Arg Glu Ala Glu Gly Glu Pro Asp
 420 425 430

 Glu Val Gly Val Asp Cys Thr Gln Leu Thr Phe Phe Pro Ala Leu His
 435 440 445

 Glu Ser Leu His Ser Glu Asp Phe Leu Glu Leu Cys Arg Glu Arg Gln
 450 455 460

 Val Ile Leu Gln Glu Leu Leu Asp Lys Glu Lys Val Thr Gln Lys Phe
 465 470 475 480

 Ser Leu Val Ile Val Gln Gly His Leu Val Ser Glu Gly Val Leu Leu
 485 490 495

 Phe Gly His Gln His Phe Tyr Ile Cys Glu Asn Phe Thr Leu Ser Pro
 500 505 510

 Thr Gly Asp Val Tyr Cys Thr Arg His Cys Leu Ser Asn Ile Ser Asp
 515 520 525

 Pro Phe Ile Phe Asn Leu Cys Ser Lys Asp Arg Ser Thr Asp His Tyr
 530 535 540

 Ser Cys Gln Cys His Ser Tyr Ala Asp Met Arg Glu Leu Arg Gln Ala
 545 550 555 560

 Arg Phe Leu Leu Gln Asp Ile Ala Leu Glu Ile Phe Phe His Asn Gly
 565 570 575

 Tyr Ser Lys Phe Leu Val Phe Tyr Asn Asn Asp Arg Ser Lys Ala Phe
 580 585 590

 Lys Ser Phe Cys Ser Phe Gln Pro Ser Leu Lys Gly Lys Ala Thr Ser
 595 600 605

 Glu Asp Thr Leu Asn Leu Arg Arg Tyr Pro Gly Ser Asp Arg Ile Met
 610 615 620

 Leu Gln Lys Trp Gln Lys Arg Asp Ile Ser Asn Phe Glu Tyr Leu Met
 625 630 635 640

 Tyr Leu Asn Thr Ala Ala Gly Arg Thr Cys Asn Asp Tyr Met Gln Tyr
 645 650 655

 Pro Val Phe Pro Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu Asn
 660 665 670

Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly Ala
 675 680 685
 Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu Val
 690 695 700
 Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His Tyr Tyr Thr His
 705 710 715 720
 Tyr Ser Ser Ala Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro Pro
 725 730 735
 Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Gly Ser Phe Asp Val Ala
 740 745 750
 Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu Ser Ala Ser Arg
 755 760 765
 Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu Phe Phe Tyr Leu
 770 775 780
 Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe Gly Cys Met Gln
 785 790 795 800
 Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro Trp Ala Asp Gly
 805 810 815
 Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser Asp
 820 825 830
 Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu Ile Phe Gly Tyr
 835 840 845
 Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His Pro
 850 855 860
 Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile Thr Asp Pro Leu
 865 870 875 880
 Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe Gly Gln Val Pro
 885 890 895
 Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr Ala Ala Gly Lys
 900 905 910
 Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser Leu Pro Gly His
 915 920 925
 Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg Pro Ser Gln Val
 930 935 940
 Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser Glu Ser Pro Lys
 945 950 955 960
 Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr Ile Leu Ala Val
 965 970 975
 Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn Arg Thr Phe Ser
 980 985 990

Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser Tyr Gly Ser Asp
 995 1000 1005
 Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys Leu
 1010 1015 1020
 Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr Ser
 1025 1030 1035 1040
 Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro Arg
 1045 1050 1055
 Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val Thr
 1060 1065 1070
 Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser Gln
 1075 1080 1085
 Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val Thr
 1090 1095 1100
 Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser Asp
 1105 1110 1115 1120
 Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu Trp
 1125 1130 1135
 Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly Pro
 1140 1145 1150
 Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp Asp
 1155 1160 1165
 Thr Ser Gln Ile Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg Val
 1170 1175 1180
 Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala Gly
 1185 1190 1195 1200
 Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp Glu
 1205 1210 1215
 Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu Thr
 1220 1225 1230
 Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val Ser
 1235 1240 1245
 Arg Asn His Thr Lys Leu Leu Val Gly Asp Glu Arg Gly Arg Ile Phe
 1250 1255 1260
 Cys Trp Ser Ala Asp Gly
 1265 1270

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 <211> 647
 <212> PRT
 <213> Homo sapiens

<400> 121

Met Leu Gln Lys Trp Gln Lys Arg Asp Ile Ser Asn Phe Glu Tyr Leu
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Met Tyr Leu Asn Thr Ala Ala Gly Arg Thr Cys Asn Asp Tyr Met Gln
20 25 30

Tyr Pro Val Phe Pro Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu
35 40 45

Asn Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly
50 55 60

Ala Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu
65 70 75 80

Val Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His Tyr Tyr Thr
85 90 95

His Tyr Ser Ser Ala Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro
100 105 110

Pro Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Gly Ser Phe Asp Val
115 120 125

Ala Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu Ser Ala Ser
130 135 140

Arg Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu Phe Phe Tyr
145 150 155 160

Leu Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe Gly Cys Met
165 170 175

Gln Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro Trp Ala Asp
180 185 190

Gly Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser
195 200 205

Asp Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu Ile Phe Gly
210 215 220

Tyr Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His
225 230 235 240

Pro Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile Thr Asp Pro
245 250 255

Leu Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe Gly Gln Val
260 265 270

Pro Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr Ala Ala Gly
275 280 285

Lys Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser Leu Pro Gly
290 295 300

His Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg Pro Ser Gln
305 310 315 320

Val Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser Glu Ser Pro
 325 330 335

 Lys Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr Ile Leu Ala
 340 345 350

 Val Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn Arg Thr Phe
 355 360 365

 Ser Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser Tyr Gly Ser
 370 375 380

 Asp Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys
 385 390 395 400

 Leu Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr
 405 410 415

 Ser Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro
 420 425 430

 Arg Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val
 435 440 445

 Thr Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser
 450 455 460

 Gln Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val
 465 470 475 480

 Thr Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser
 485 490 495

 Asp Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu
 500 505 510

 Trp Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly
 515 520 525

 Pro Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp
 530 535 540

 Asp Thr Ser Gln Ile Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg
 545 550 555 560

 Val Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala
 565 570 575

 Gly Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp
 580 585 590

 Glu Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu
 595 600 605

 Thr Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val
 610 615 620

Ser Arg Asn His Thr Lys Leu Leu Val Gly Asp Glu Arg Gly Arg Ile
625 630 635 640

Phe Cys Trp Ser Ala Asp Gly
645

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amplification primer PDM-797

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gtqtcacaat ctacagtcaq qcaggattct cc 32

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amplification primer PDM-799

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<211> 980
<212> DNA
<213> *Homo sapiens*

<400> 124
ggcgcgtgccg ctcccaggaga caggttcccc tgcaggaatg aaagacatgg aagggaagag 60
ggggggccagc tcccttgagtc ctgtgtccac cagctgctgc taaataacctc tgagaaactc 120
tgcttctatc taaggggacc tactttctc gggaatctca atacttggaa caagaacctc 180
ctagacggac ccttggcat aatgaattgg accaactgtt ggttccagga cttagagagcc 240
agcaatgcct ccatgaacaa tctcacccaa ttactctgtt cagggaaacgaa ggtaactgtat 300
ggacagccga ggcagccct taggcccgtt aggccctcccc tgtggagcat ccctgaggcg 360
gactccggcc agcccgagtg atgcgtatcca aagagcaccc ccgggttagga aattgccccg 420
gttggaaatgcc tcaccagagc agcgtgttagc agttccctgtt ggaggattaa cacagtggct 480
gaacaccggg aaggaactgg cacttggagt ccggacatct gaaacttgta gactgggagc 540
tgtacatggc tgggagcagc ttcaccaacc cctgcaaagt gactctgaag aagacgacaa 600
gccctgtcc agtcacaccc ggaagctgac tggccacgc acagctgaag catgagaaa 660
ctcatcgccg gactaatttt cttaaaatt tagacttgta cagtaaggac ttcaactgac 720
cttcctcaga ctgagaactg ttccagtat atacatcaag tcactgaggt aggacaaaag 780
attgctacat tcctattatt ttaaggttac atttttgggg acccctctt cttctgttct 840
agctattacc ttctttgtgt cacctagaaa aggaccagtc cttaaattgtt tttaaaaaac 900
tgtgtatcatg ggaagcttta aattggttca ataacacgca tcaagttggt tatttcctgg 960
gctacatacc ttggatagat 980

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